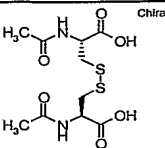
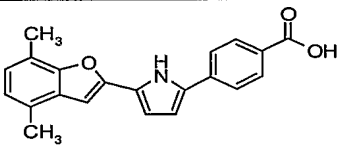
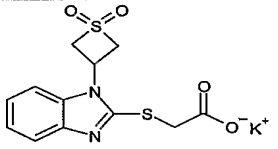
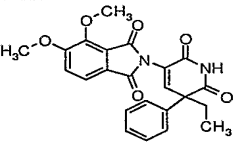
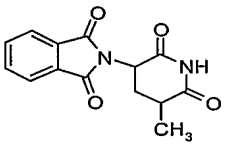
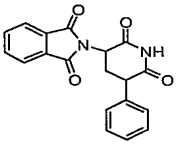
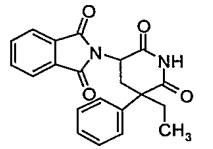
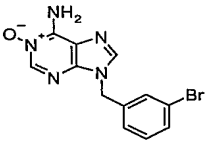
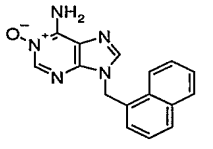
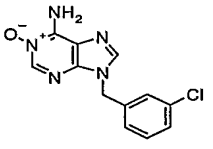
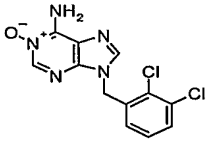
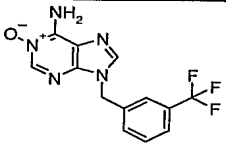
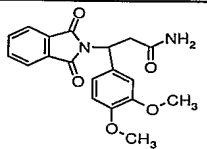
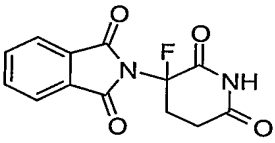
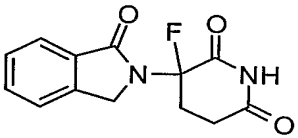
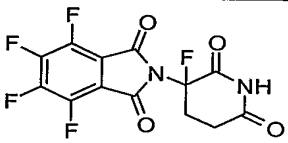
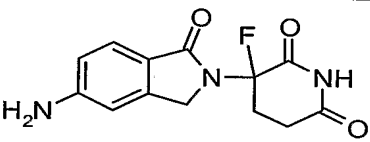
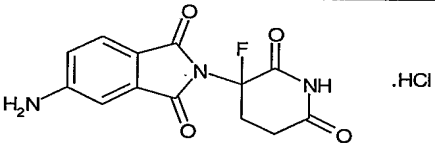
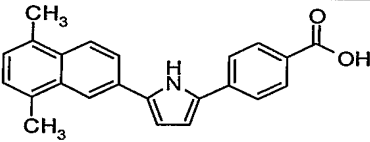
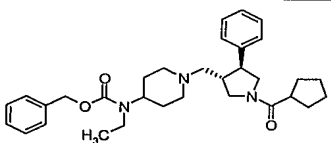
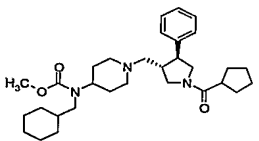
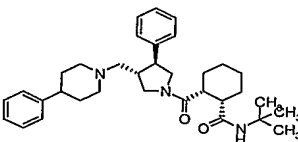
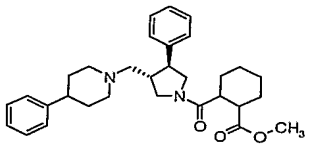
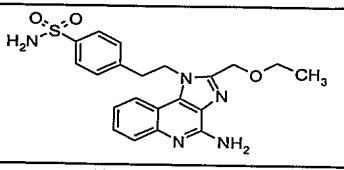
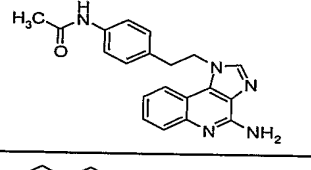
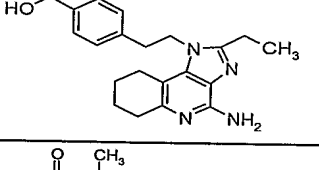
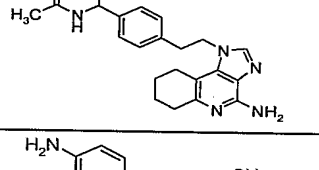
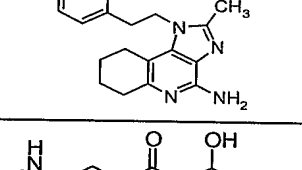
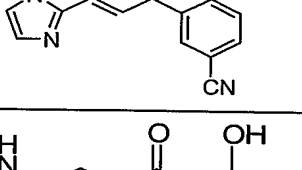
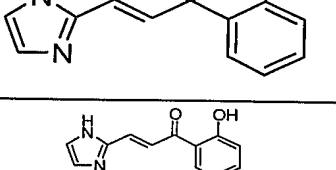
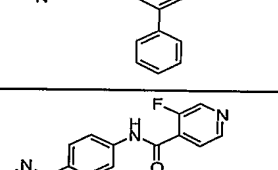
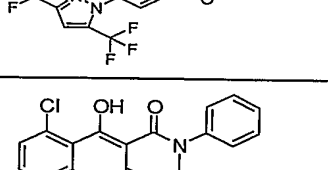
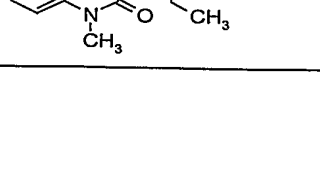
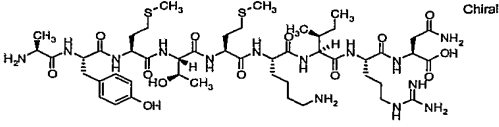
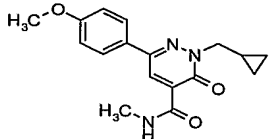
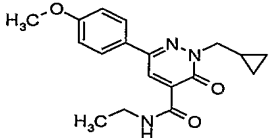
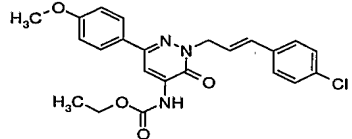
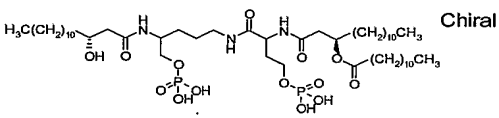
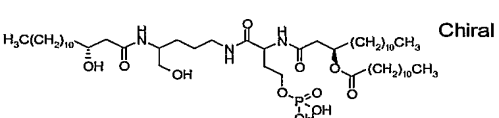
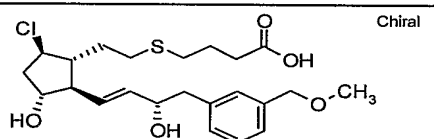
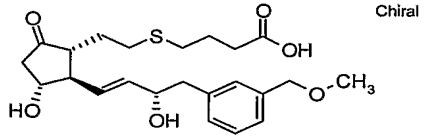
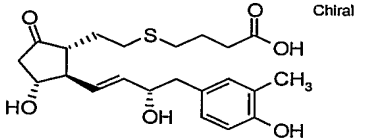
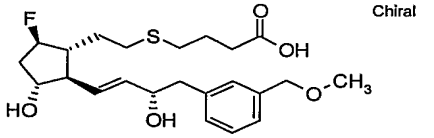
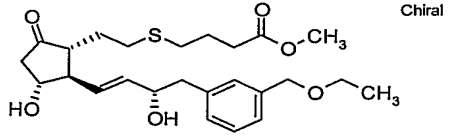
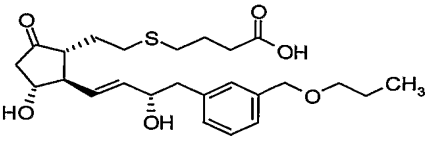
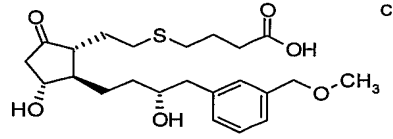
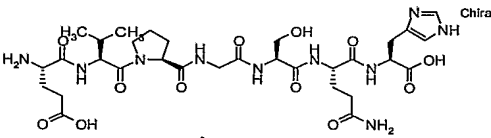
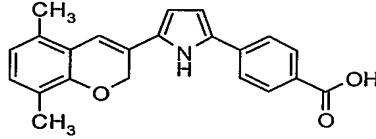
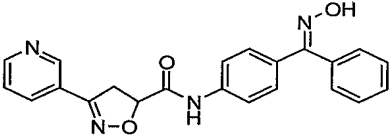
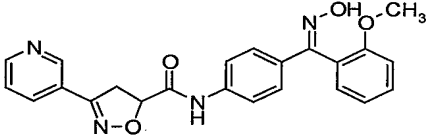
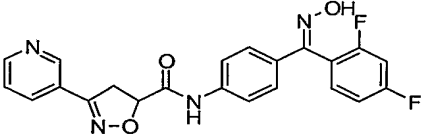
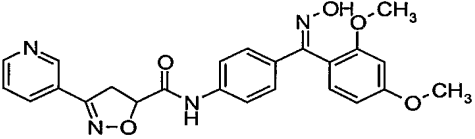
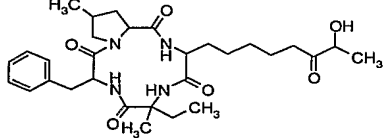
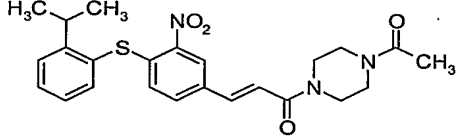
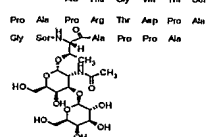


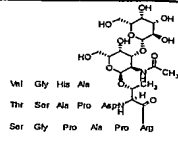
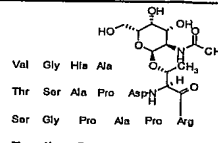
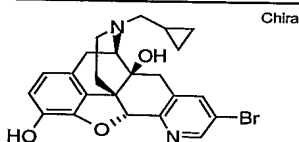
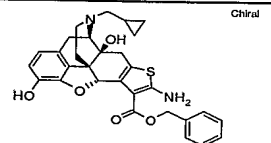
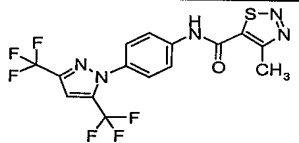
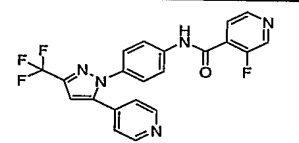
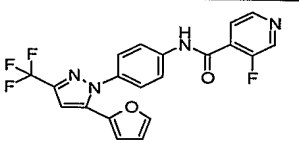
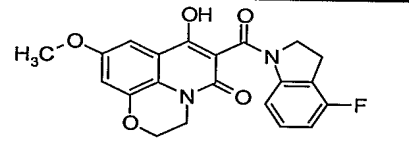
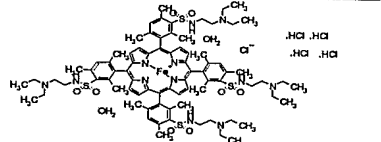
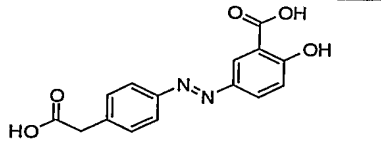
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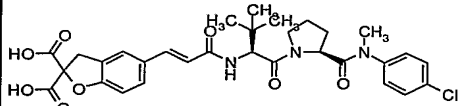
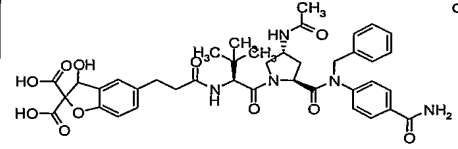
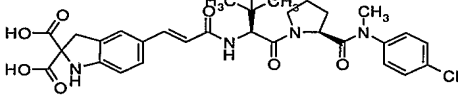
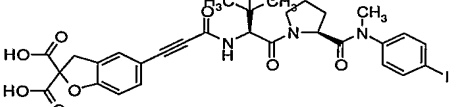
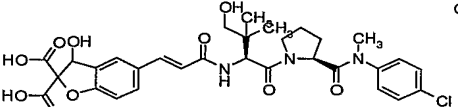
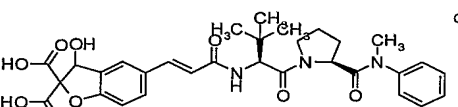
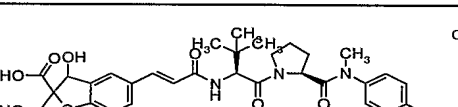
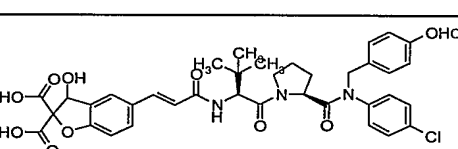
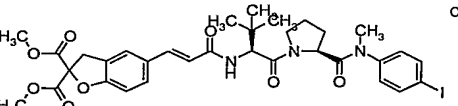
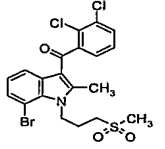
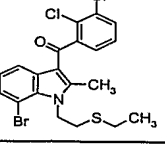
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1158		Eisai	Hibi, S. et al. Bioorg Med Chem Lett 2000, 10(7): 623.	EP 0889032
1159		Janssen		WO 0021959
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1165	 Ala His Gly Val Thr Ser Pro Ala Pro Arg Thr Asp Pro Ala Gly Ser-His-Ala-Pro-Pro-Ala	Cancer Research UK		WO 0052046

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1170		Abbott Labs.	EP 1068187
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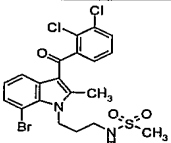
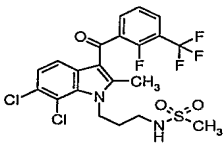
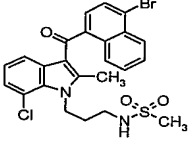
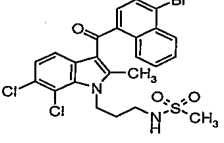
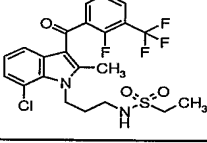
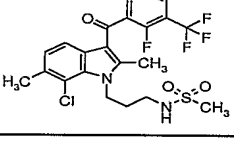
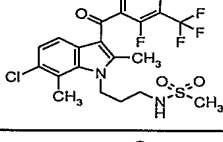
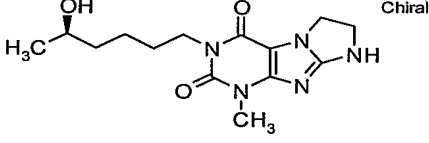
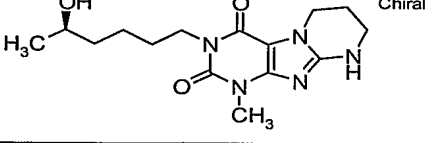
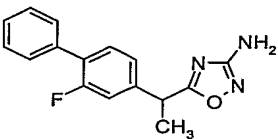
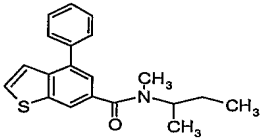
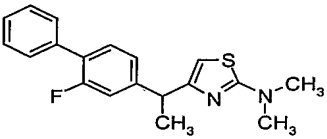
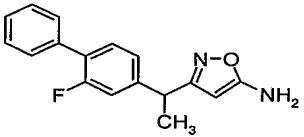
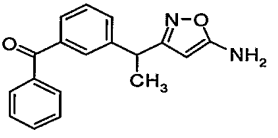

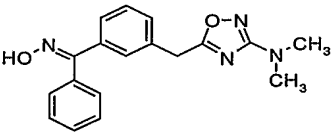
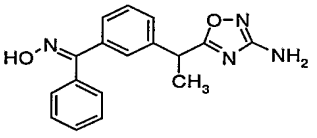
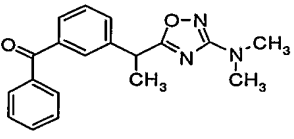
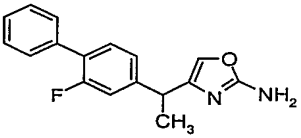
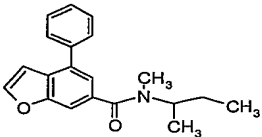
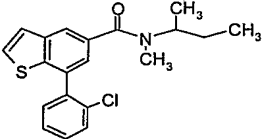
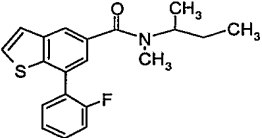
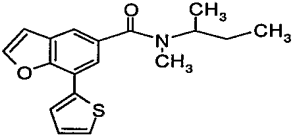
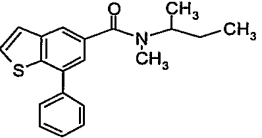
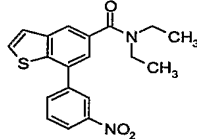
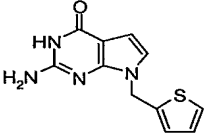
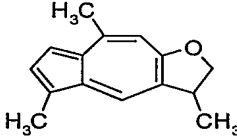
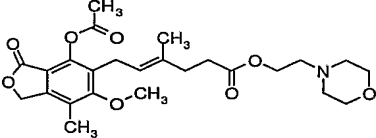
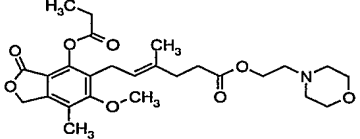
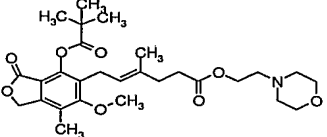
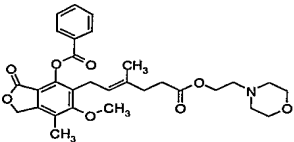
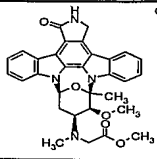
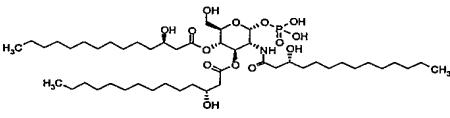
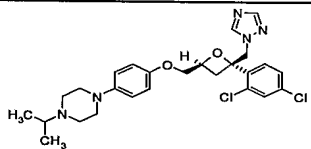
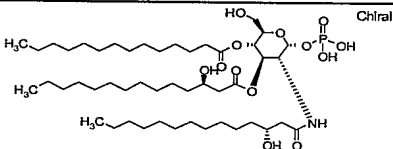
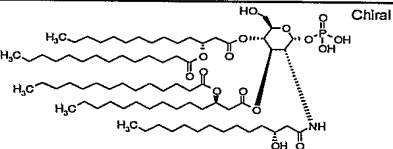
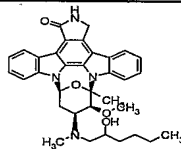
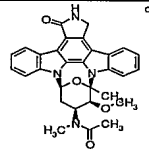
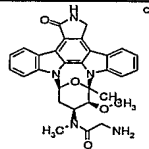
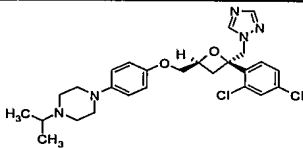
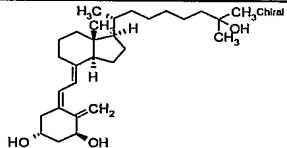
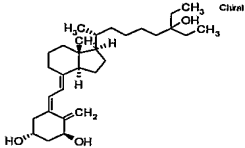
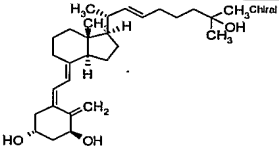
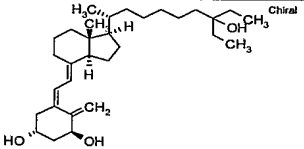
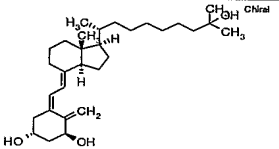
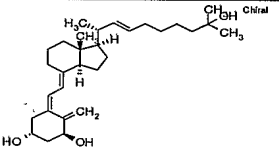
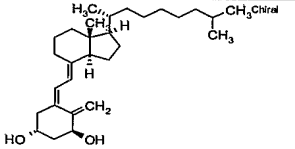
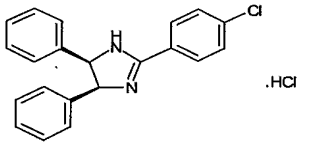
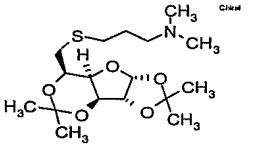
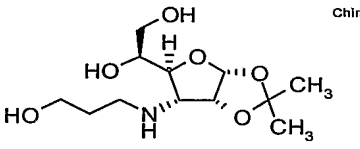
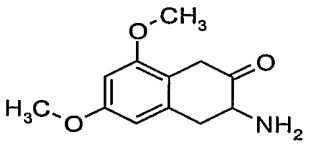
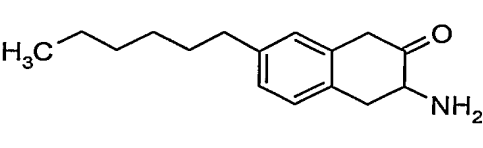
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1191		Sanofi-Synthelabo		WO 0242269
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1193		Sanofi-Synthelabo		WO 0242269
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1196	 Chiral	Cell Therapeutics		WO 0268421

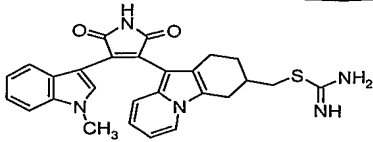
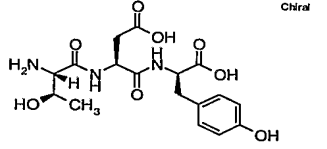
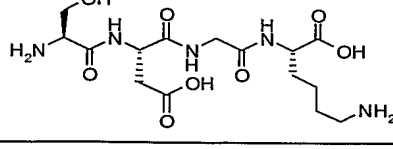
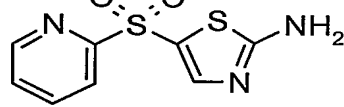
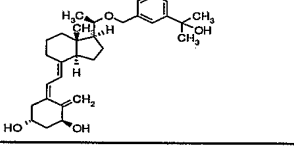
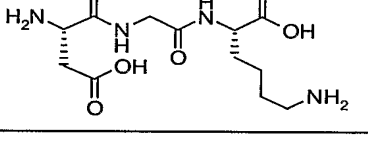
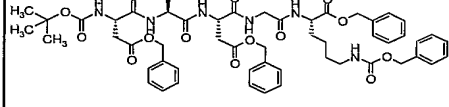
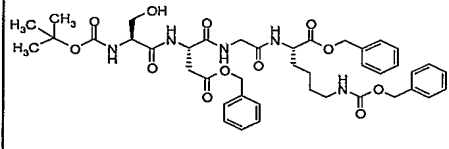
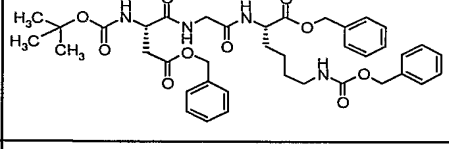
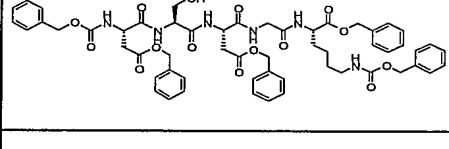
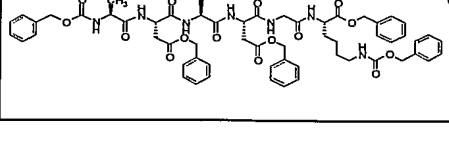
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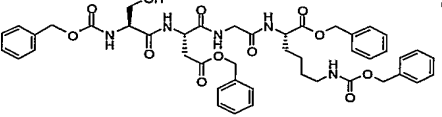
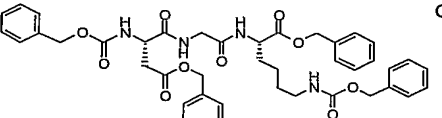
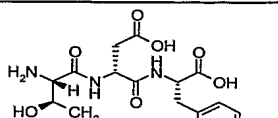
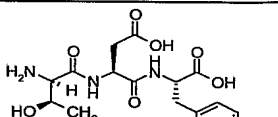
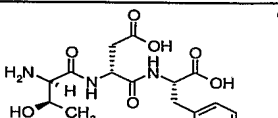
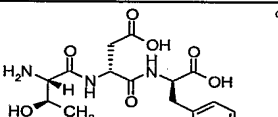
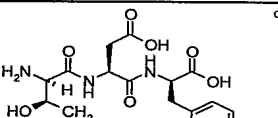
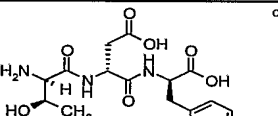
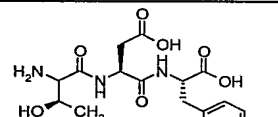
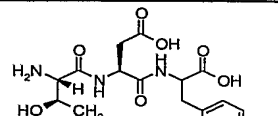
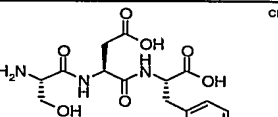
Compound #	Structure	Source	Literature Reference	Patent Number
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1198		Aventis Pharma		EP 248734
1199		Sumitomo Pharmaceuticals		EP 248399
1200		Sumitomo Pharmaceuticals		EP 248399
1201		Sumitomo Pharmaceuticals		EP 248399
1202		Sumitomo Pharmaceuticals		EP 248399
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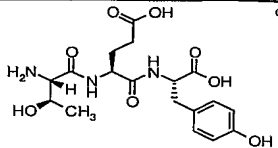
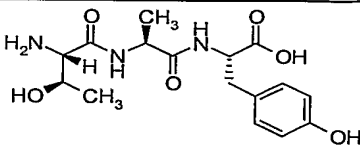
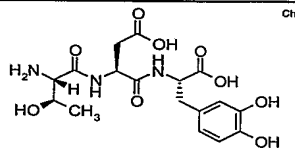
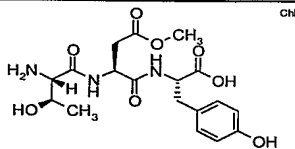
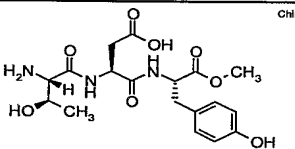
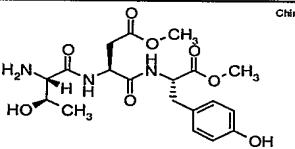
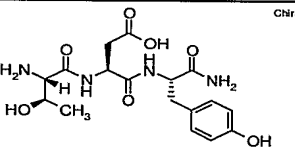
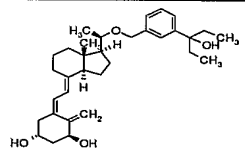
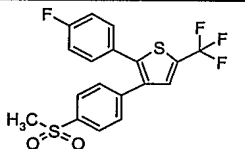
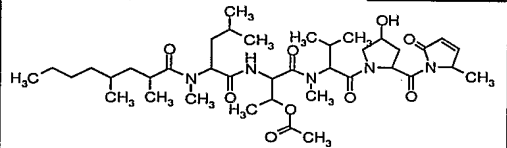
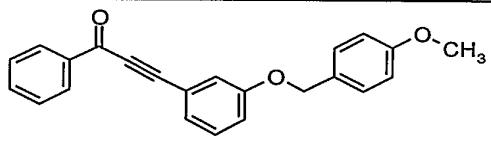
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1211		Aventis Pharma	EP 248734
1212		Aventis Pharma	EP 248734
1213		Pfizer	AU 8783281
1214		Harbor Branch Found.	US 4755529
1215		Roche Bioscience	AU 8782540
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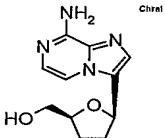
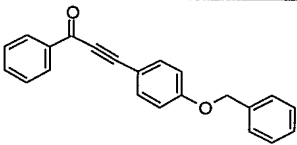
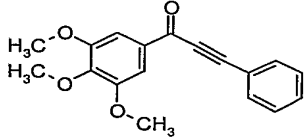
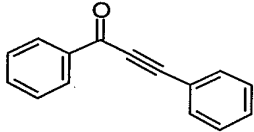
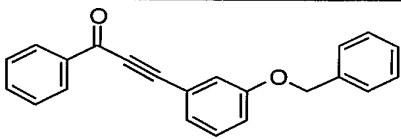
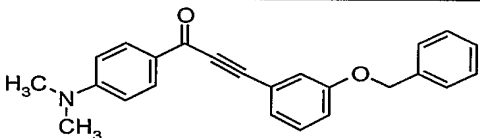
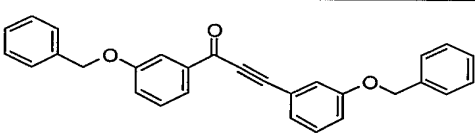
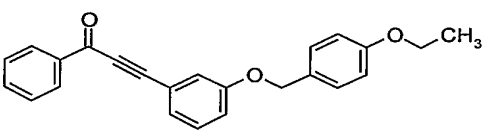
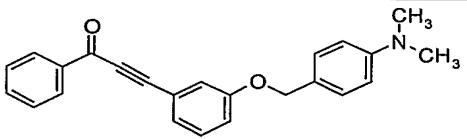
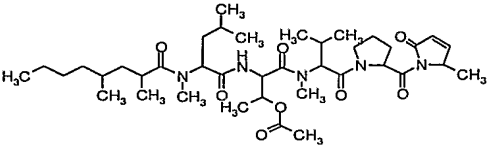
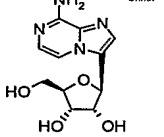
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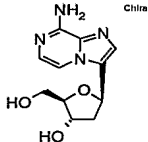

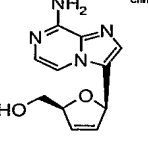
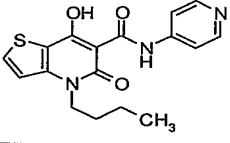
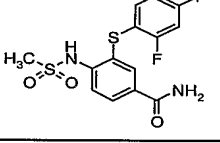
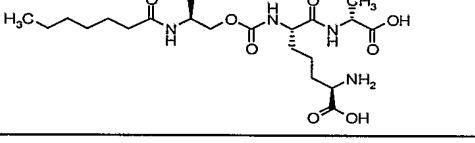
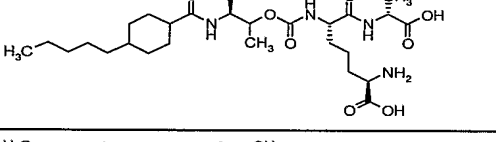
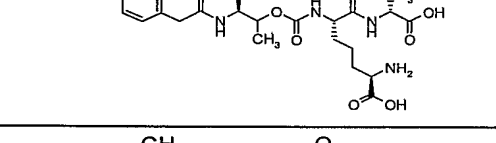
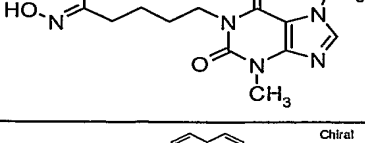
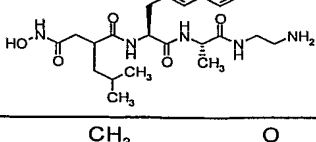
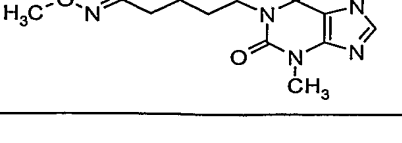
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1235		Tanabe Seiyaku	1) Ueno, M. et al. Jpn J Pharmacol 1992, 58(Suppl. 1): Abst O-210.	AU 8942368
1236		Greenwich Pharm.		AU 9047648
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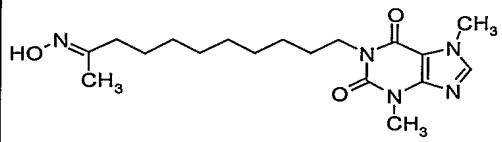
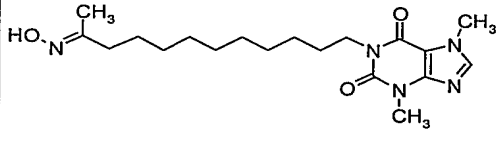
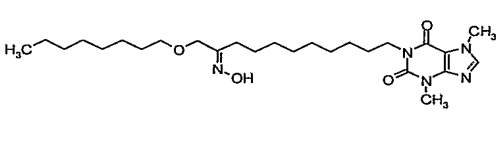
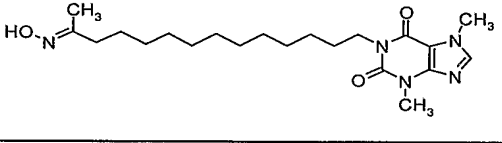
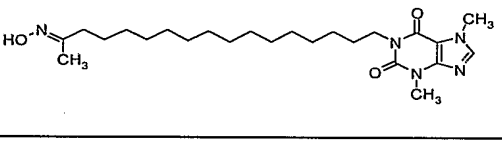
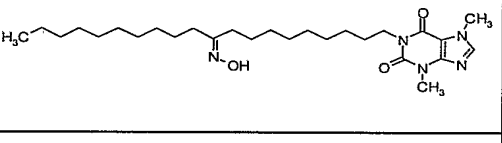
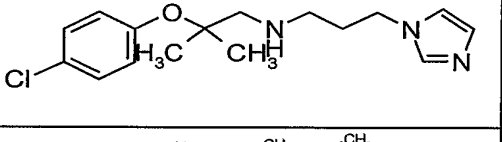
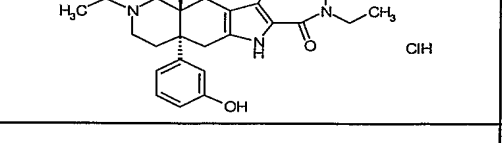
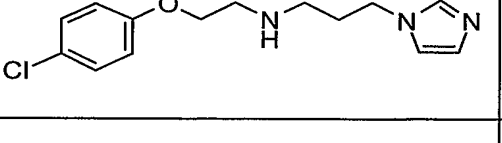
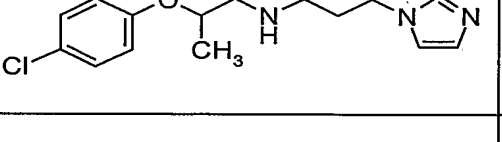
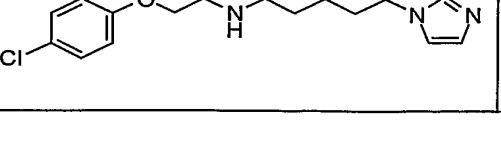
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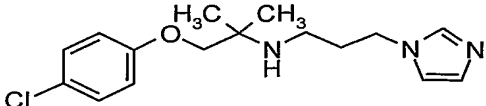
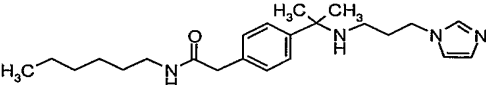
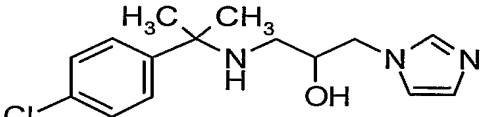
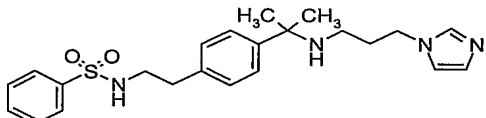
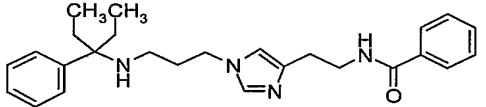
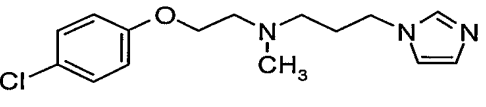
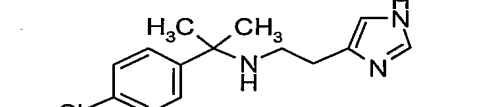
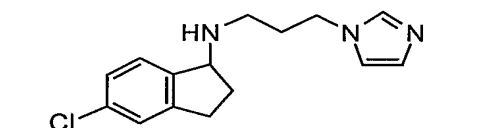
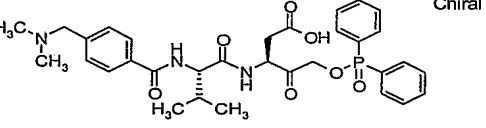
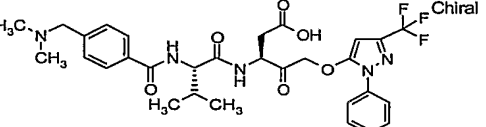
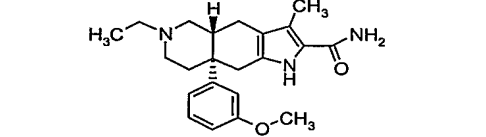
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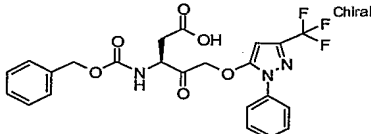
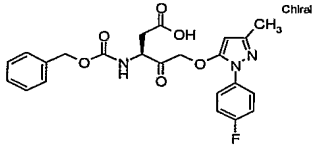
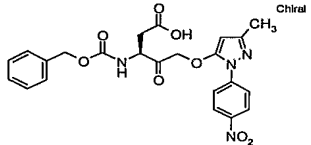
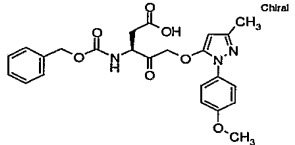
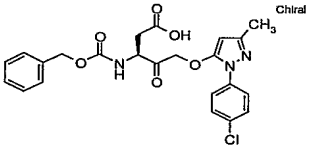
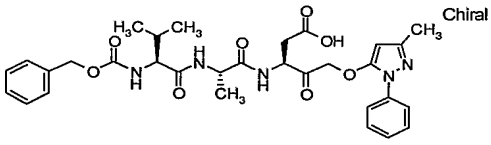
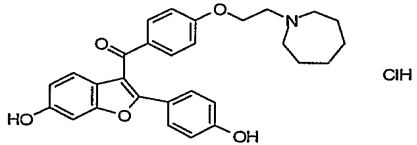
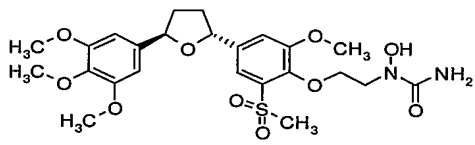
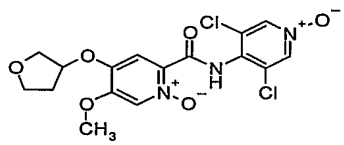
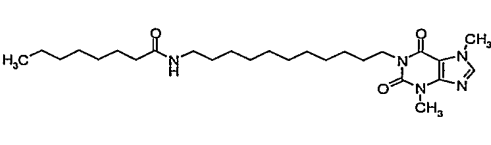
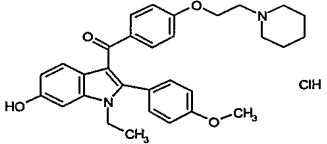
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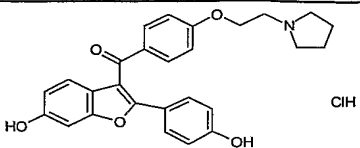
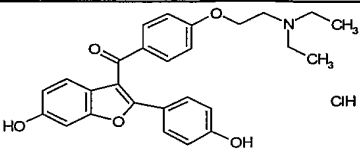
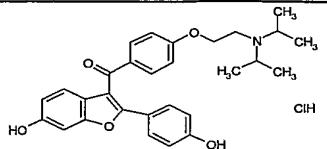
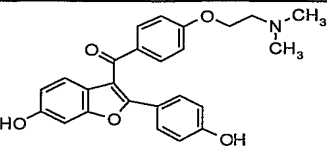
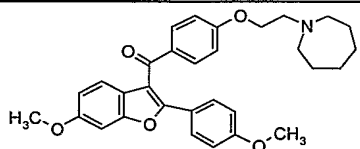
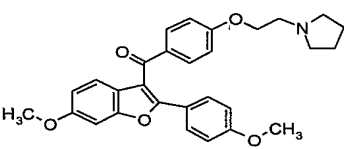
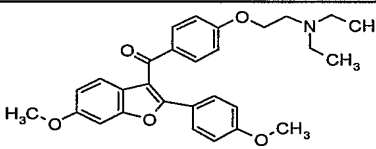
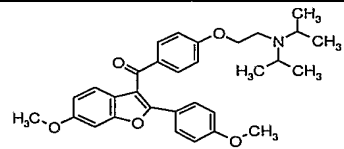
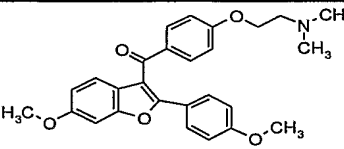
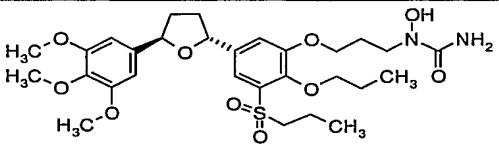
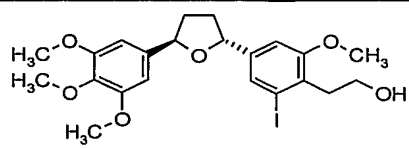
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1288		Fujisawa	Nakamura, K. et al. Chem Pharm Bull 1993, 41(5): 894.	AU 8783152
1289		Wyeth		US 5312831
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1293		Immunex	1) Immunex Corporation Press Release 1994, July 21.	WO 9506031
1294		Cell Therapeutics		WO 9416704

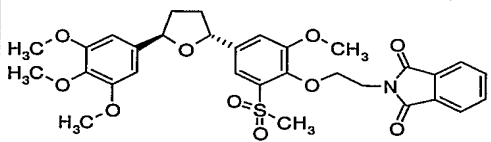
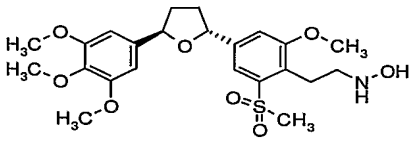
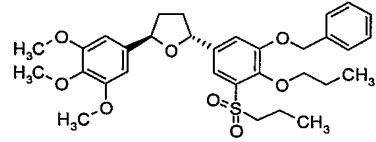
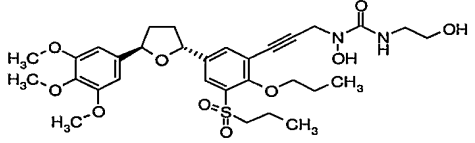
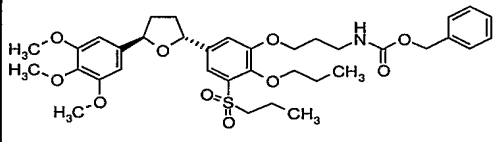
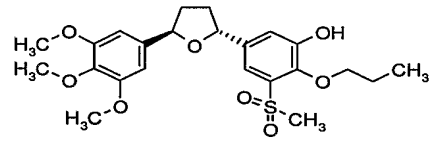
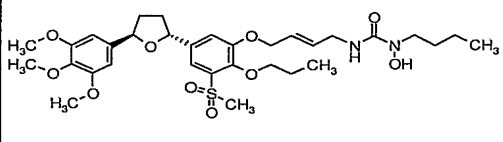
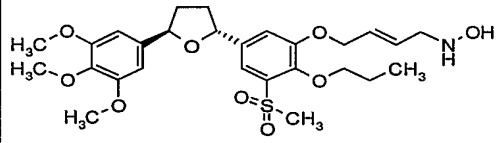
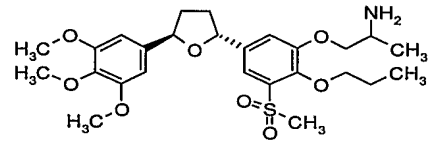
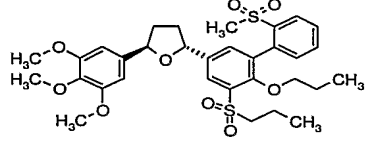
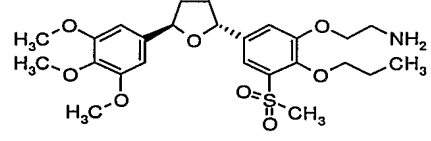
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1307		Abbott GmbH	WO 9500493
1308		Abbott GmbH	WO 9500493
1309		Abbott GmbH	WO 9500493
1310		Abbott GmbH	WO 9500493
1311		Abbott GmbH	WO 9500493
1312		Abbott GmbH	WO 9500493
1313		Abbott GmbH	WO 9500493
1314		Sanofi-Synthelabo	EP 644197
1315		Sanofi-Synthelabo	CA 2125021
1316		GlaxoSmithKline	WO 9504734

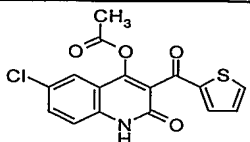
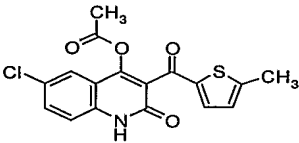
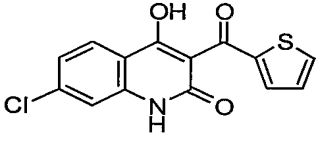
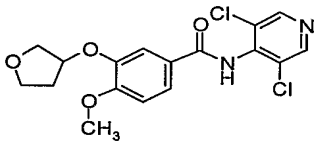
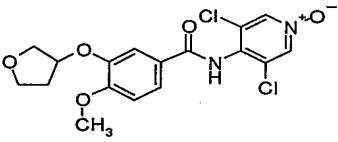
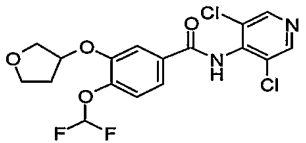
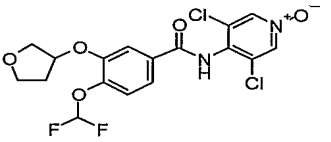
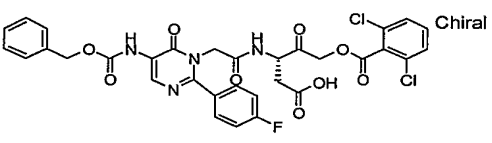
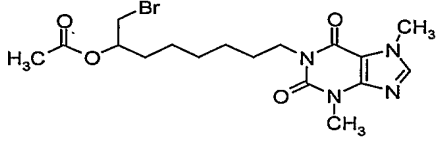
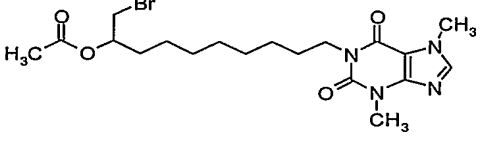
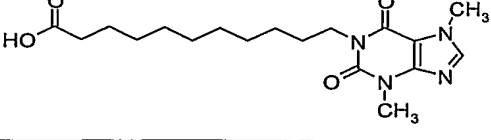
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1320		GlaxoSmithKline		WO 9504734
1321		GlaxoSmithKline		WO 9504734
1322		Japan Tobacco		JP 95002779
1323		Pharmacia	1) Gozzi, P. et al. J Pharmacol Exp Ther 1999, 291(1): 199.	JP 1995501330
1324		Sanofi-Synthelabo	Chiral	EP 644197
1325		Sanofi-Synthelabo	Chiral	EP 644197
1326		Sanofi-Synthelabo	Chiral	EP 644197
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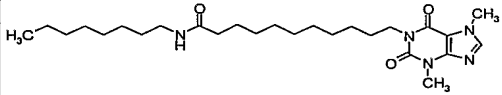
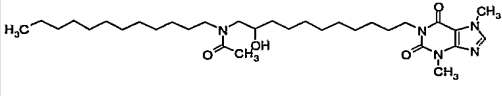
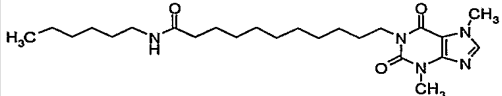
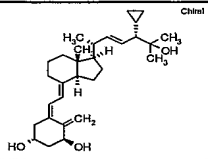
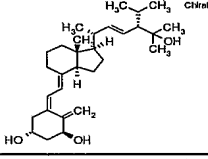
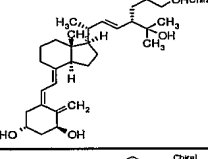
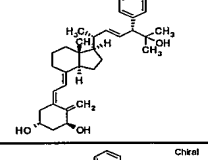
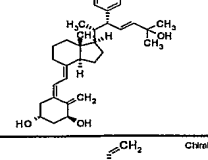
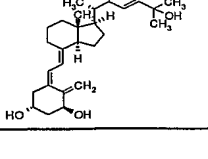
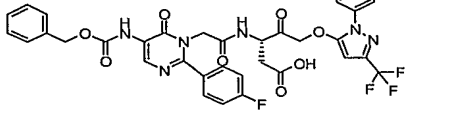
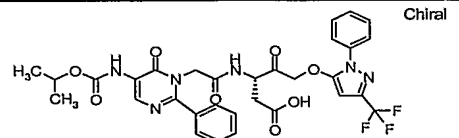
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1332		Sanofi-Synthelabo	CA 2125021
1333		Sanofi-Synthelabo	CA 2125021
1334		Lilly	WO 9517382
1335		Millennium	WO 9518610
1336		Aventis Pharma	WO 9520578
1337		Cell Therapeutics	WO 9522546
1338		Lilly	WO 9517382

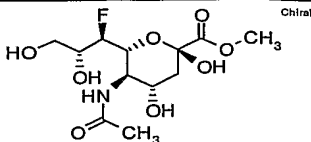
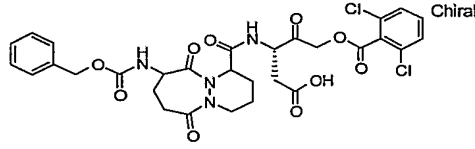
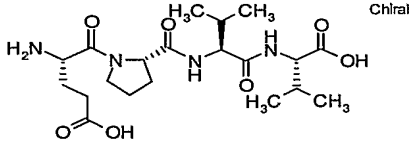
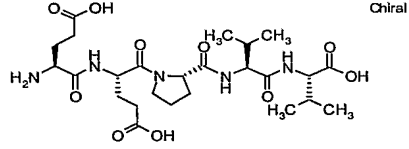
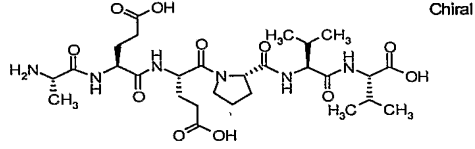
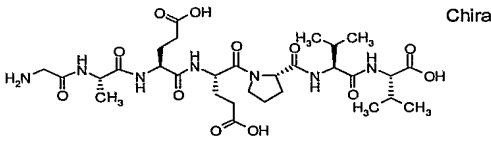
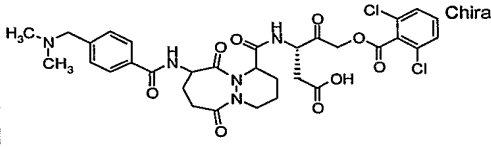
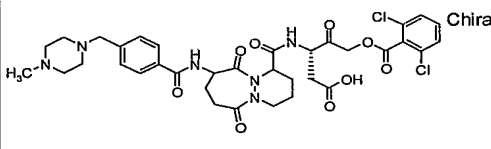
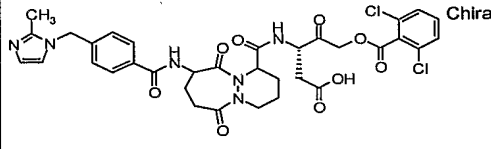
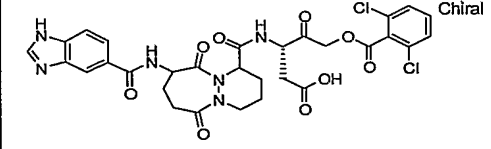
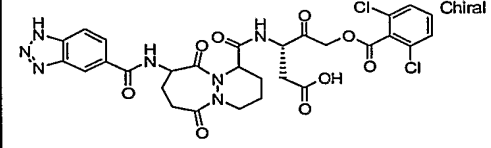
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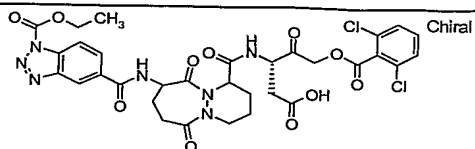
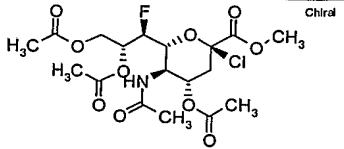
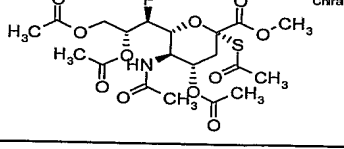
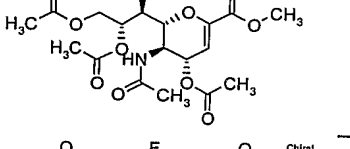
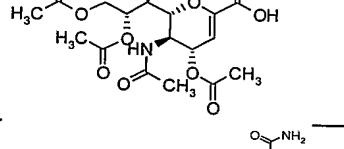
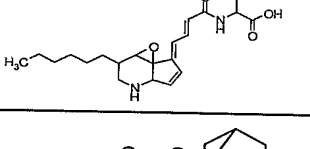
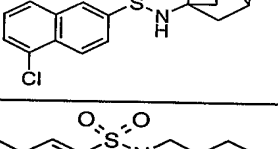
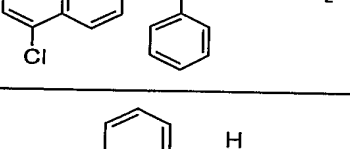
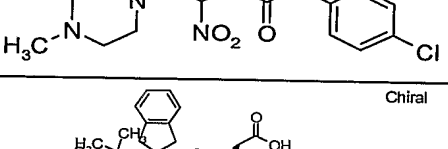
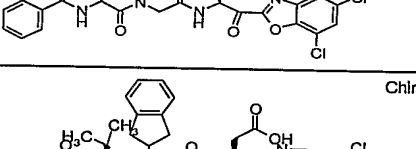
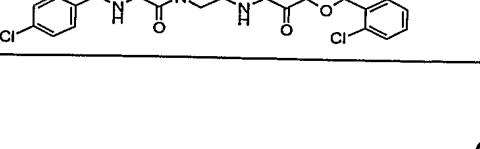
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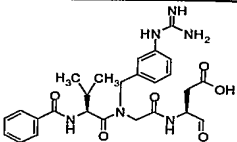
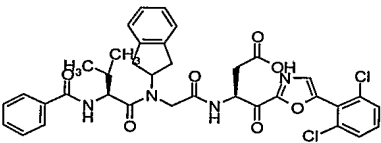
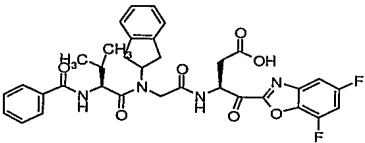
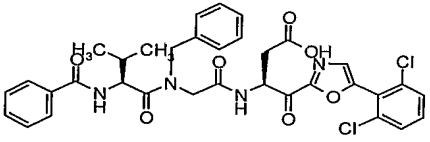
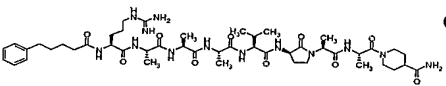
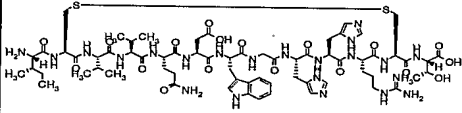
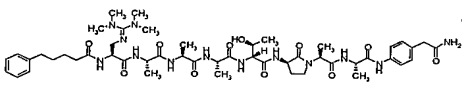
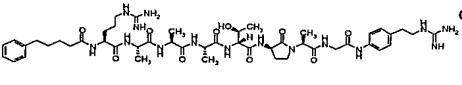
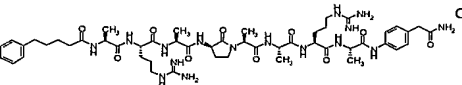
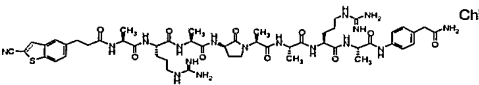
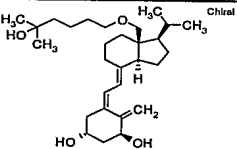
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1366		Duphar	EP 664287
1367		Japan Tobacco	JP 95002779
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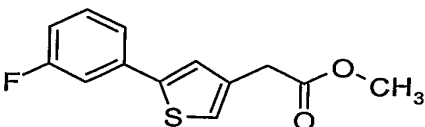
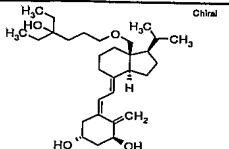
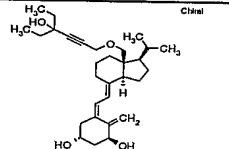
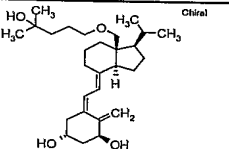
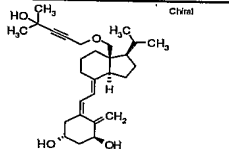
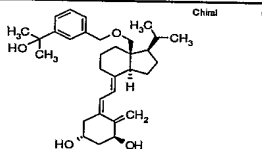
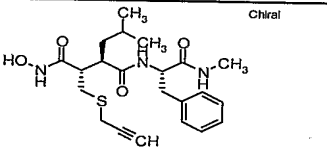
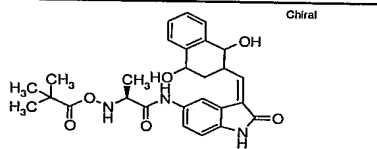
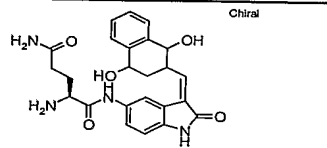
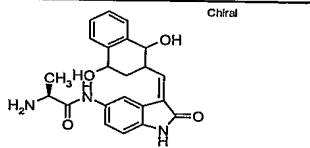
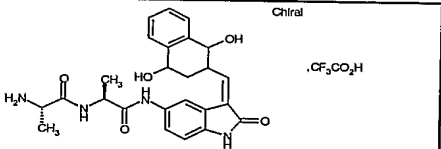
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1379		Sanofi-Synthelabo	WO 9526958
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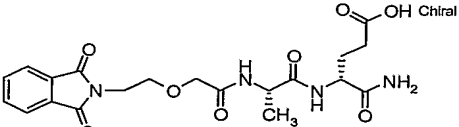
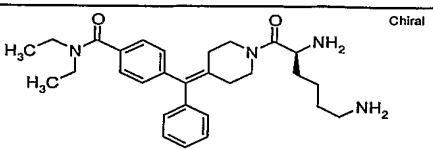
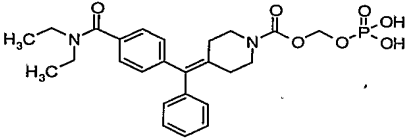
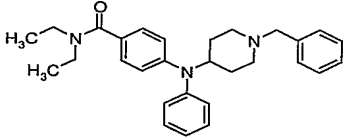
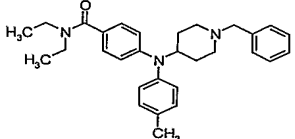
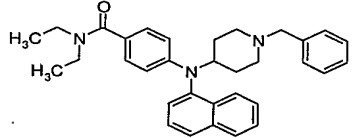
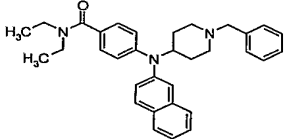
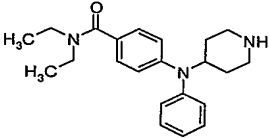
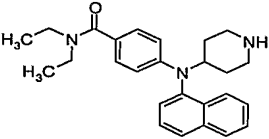
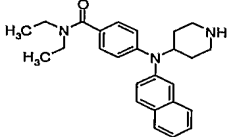
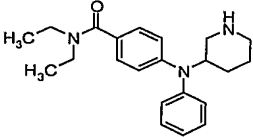
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1390		Duphar	EP 664287
1391		Duphar	EP 664287
1392		Sanofi-Synthelabo	WO 9526958
1393		Sanofi-Synthelabo	WO 9526958

1394	 Chiral	Daikin	EP 711766
1395	 Chiral	Sanofi-Synthelabo	WO 9533751
1396	 Chiral	Ajinomoto	US 5464819
1397	 Chiral	Ajinomoto	US 5464819
1398	 Chiral	Ajinomoto	US 5464819
1399	 Chiral	Ajinomoto	US 5464819
1400	 Chiral	Sanofi-Synthelabo	WO 9533751
1401	 Chiral	Sanofi-Synthelabo	WO 9533751
1402	 Chiral	Sanofi-Synthelabo	WO 9533751
1403	 Chiral	Sanofi-Synthelabo	WO 9533751
1404	 Chiral	Sanofi-Synthelabo	WO 9533751

1405		Sanofi-Synthelabo		WO 9533751
1406		Daikin		EP 711766
1407		Daikin		EP 711766
1408		Daikin		EP 711766
1409		Daikin		EP 711766
1410		Microbial Chemistry Research Foundation		JP 96176157
1411		Tanabe		WO 9640641
1412		Tanabe		WO 9640641
1413		Daiichi Pharmaceutical	1) Kawagoe, K. et al. AFMC Int Med Chem Symp (Sept 3-8, Tokyo) 1995, Abst P13M183.	JP 97059236
1414		Vertex		WO 9722618
1415		Vertex		WO 9722618

1416	 Chiral	Vertex		WO 9722618
1417	 Chiral	Vertex		WO 9722618
1418	 Chiral	Vertex		WO 9722618
1419	 Chiral	Vertex		WO 9722618
1420	 Chiral	AstraZeneca		WO 9731023
1421	 Chiral	University of Pennsylvania		WO 9733603
1422	 Chiral	AstraZeneca		WO 9731023
1423	 Chiral	AstraZeneca		WO 9731023
1424	 Chiral	AstraZeneca		WO 9731023
1425	 Chiral	AstraZeneca		WO 9731023
1426	 Chiral	Leo		WO 9737972

1427		Taisho		JP 97194476
1428		Leo		WO 9737972
1429		Leo		WO 9737972
1430		Leo		WO 9737972
1431		Leo		WO 9737972
1432		Leo		WO 9737972
1433		GlaxoSmithKline		WO 9743250
1434		Pharmacia		WO 9745409
1435		Pharmacia		WO 9745409
1436		Pharmacia		WO 9745409
1437		Pharmacia		WO 9745409

1438		LEK		EP 477912
1439		AstraZeneca		WO 9828275
1440		AstraZeneca		WO 9828275
1441		AstraZeneca		WO 9828270
1442		AstraZeneca		WO 9828270
1443		AstraZeneca		WO 9828270
1444		AstraZeneca		WO 9828270
1445		AstraZeneca		WO 9828270
1446		AstraZeneca		WO 9828270
1447		AstraZeneca		WO 9828270
1448		AstraZeneca		WO 9828270

1449		AstraZeneca	WO 9828270
1450		AstraZeneca	WO 9828270
1451		AstraZeneca	WO 9828270
1452		AstraZeneca	WO 9828270
1453		AstraZeneca	WO 9828270
1454		AstraZeneca	WO 9828270
1455		AstraZeneca	WO 9828270
1456		AstraZeneca	WO 9828270
1457		AstraZeneca	WO 9828270
1458		AstraZeneca	WO 9828270
1459		Daiichi Pharmaceutical	Koiwa, T. et al. J Antibiot 1999, 52(2): 198.

1460	 Chiral	Bristol-Myers Squibb	WO 0244181
1461		Bristol-Myers Squibb	WO 0244181
1462		Bristol-Myers Squibb	WO 0244181
1463	 Chiral	Bristol-Myers Squibb	WO 0244181
1464	 Chiral	Bristol-Myers Squibb	WO 0244181
1465		Bristol-Myers Squibb	WO 0244181
1466		Bristol-Myers Squibb	WO 0244181
1467	 Chiral	Bristol-Myers Squibb	WO 0244181
1468		Bristol-Myers Squibb	WO 0244181
1469		Gruenenthal	WO 0290317

BRIEF DESCRIPTION OF SEQUENCE LISTING

SEQ ID NO:	Description
1	Draft genome assembly from The Genome Science Center in British Colombia, Canada of sequence from TOR2 isolate. <i>TOR2_draft_genome_assembly_120403 Release 1</i>
2	CDC SARS-CoV strain sequence. Entire nucleotide sequence (Urbani strain)
3-20	Group-specific coronavirus gene products > Feline infectious peritonitis virus (FIPV) 3/4 = ORF 3b; 5/6 = ORF 3X; 7/8 = ORF 3A > Canine coronavirus 9/10 = ORF 7b; 11/12 = ORF 7a > Avian infectious bronchitis virus 13/14 = ORF 5b; 15/16 = ORF 5a; 17/18 = ORF 3a; 19/20 = ORF 3b
21-520	500 primers for left part
521-1020	500 primers for right part
1021-3520	Forward primers from Table 4
3521-6020	Reverse primers from Table 4
6021-6026	Figure 9 primers
6027-6033	Figure 11 primers
6034-6038	Five primers from http://content.nejm.org/cgi/reprint/NEJMoa030781v2.pdf
6039-6051	PEP1 to PEP13
6052	Extended PEP13
6053-6056	229E human coronavirus sequences
6057-6060	TGV sequences
6061-6064	PEDV sequences
6065-6068	Bovine coronavirus sequences
6069-6071	Murine hepatitis virus sequences
6072-6075	AIBV sequences
6076-6170	Primer sequences (forward)
6171-6265	Primer sequences (reverse)
6266-6304	Primer sequences (forward)
6305-6343	Primer sequences (reverse)
6344-6366	Primer sequences (forward)
6367-6392	Primer sequences (reverse)
6393-6440	Primer sequences (forward) F1-F48
6441-6487	Primer sequences (reverse) R1-R47
6488-6559	Primer sequences
6560-6568	Primer sequences
6569	The nsp2 proteinase (3CL-PRO) sequence in SARS coronavirus
6570-72	The nsp2 proteinases (3CLp) of avian IBV, MHV, and BCoV
6573	Consensus nsp2 proteinases sequence
6574-6577	IG sequences from Figure 18
6578	Expression construct of nSh in pCMVIII
6579	Expression construct of nS in pCMVIII
6580	Expression construct of nSh ΔTC in pCMVIII
6581	Expression construct of nS ΔTC in pCMVIII
6582	Expression construct of nS1h in pCMVIII
6583	Expression construct of nS1 in pCMVIII
6584-6585	Primers for cDNA amplification
6585-6587	Primers for RT-PCR
6588-6809	Component sequences of Figure 23 (≥4 amino acids)
6810-7179	Component sequences of Figure 24 (≥4 amino acids)
7180-7187	N-glycosylation sites within SEQ ID NO: 6039
7188-7189	Component sequences of Figure 25
7190	Fragment of SEQ ID NO: 7188
7191	Polynucleotide encoding SEQ ID NO: 7190
7192	Amino acids 879-1005 of SEQ ID NO: 6042
7193	Amino acids 879-980 of SEQ ID NO: 6042

7194	Amino acids 901-1005 of SEQ ID NO: 6042
7195	Amino acids 1144-1201 of SEQ ID NO: 6042
7196	Amino acids 1144-1196 of SEQ ID NO: 6042
7197-7199	Membrane fusion peptide regions
7200-7206	NadA-based polypeptides
7207-7223	N-glycosylation sites within SEQ ID NO: 6042
7224-7231	Slippage region
7232	Orf1ab polypeptide
7233-7244	Orf1ab polypeptides
7245-7247	X ₂ sequences for SEQ ID NOS 7233-7244
7248-7253	Orf1ab polypeptides
7254	Zinc binding region 2 site
7255-7271	N-glycosylation sites in SEQ ID NOS: 6040-41,6043,6045-46,6050-51
7272-7291	Polypeptides and polynucleotides
7292-7293	Intergenic sequences
7294-7301	Nucleotides from 5' end of SARSV genome followed by intergenic sequence
7302-7306	NadA constructs
7307-7308	Fragments of SEQ ID NO: 6042
7309	NadA sequence
7310-7311	NadA leader sequences
7312-7315	Amino acid sequences from NadA
7316-7324	PCR primers
7325-7330	Primers
7331	CCACC sequence
7332-7336	3' UTR forward primers
7337-7341	3' UTR reverse primers
7342-7352	3' UTR probes
7353-7362	5' UTR forward primers
7363-7373	5' UTR reverse primers
7374-7385	5' UTR probes
7386	Conserved octanucleotide
7387	Reverse complement of SEQ ID NO: 7293
7388	Intergenic sequence
7389	Poly T
7390	Stem-loop sequence
7391-7392	Poly-glycine linkers
7393	Poly-histidine tag
7394	Nucleocapsid epitope site
7395	Antisense primer
7396-7397	Probes
7398-7399	Antigenic fragments of SEQ ID NO: 6042
7400-7639	T-epitope analysis of SEQ ID NO: 6039
7640-7800	T-epitope analysis of SEQ ID NO: 6040
7801-8040	T-epitope analysis of SEQ ID NO: 6041
8041-8280	T-epitope analysis of SEQ ID NO: 6042
8281-8486	T-epitope analysis of SEQ ID NO: 6043
8487-8665	T-epitope analysis of SEQ ID NO: 6044
8666-8820	T-epitope analysis of SEQ ID NO: 6045
8821-9018	T-epitope analysis of SEQ ID NO: 6046
9019-9131	T-epitope analysis of SEQ ID NO: 6047
9132-9308	T-epitope analysis of SEQ ID NO: 6048
9309-9437	T-epitope analysis of SEQ ID NO: 6049
9438-9538	T-epitope analysis of SEQ ID NO: 6050
9539-9752	T-epitope analysis of SEQ ID NO: 6052
9753-9763	Primers for spike protein amplification, particularly fragments of spike
9764-9765	N-glycosylation sites within SEQ ID NO: 6039
9766-9779	Cleavage products for ORF1ab (Table 10)

9780-9782	Forward primer, reverse primer, probe
9783-9784	Lysine-rich region
9785-9798	Oligonucleotides used for <i>S.cerevisiae</i> expression
9799-9802	Sequences from Figures 65 & 66
9803-9882	Primers for <i>E.coli</i> cloning
9883-9885	BCV nucleotide sequences for Figures 3A, 3B, 3C
9886-9891	BCV amino acid sequences for Figures 4A, 4B, 4C, 4D, 4E, 4F
9892	BCV 5' UTR
9893	BCV 3' UTR
9894-9896	MHV nucleotide sequences for Figures 3A, 3B, 3C
9897-9902	MHV amino acid sequences for Figures 4A, 4B, 4C, 4D, 4E, 4F
9903-9904	AIBV nucleotide sequences for Figures 3A, 3B
9905-9909	AIBV amino acid sequences for Figures 4A, 4B, 4D, 4E, 4F
9910	AIBV 5' UTR
9911	AIBV 3' UTR
9912-9913	HOBMPRO, HOBHEGA nucleotide sequences for Figures 3B, 3C
9914-9918	Human CoV amino acid sequences for Figures 4A, 4B, 4C, 4E, 4F
9919	HCoV-OC43 5' UTR
9920	HCoV-OC43 3' UTR
9921-9923	pCMVKm2 vectors
9924-9926	Codon-optimised N, M and E sequences
9927	BNI-1
9928-9959	Constituent amino acid sequences ≥ 4 aa inferred from SEQ ID NO: 9927
9960	ORF1ab variant
9961	ORF1a variant
9962	Spike variant
9963	Membrane variant
9964	Nucleocapsid variant
9965-9966	Short ORFs
9967	FRA complete genome

CLAIMS

1. An isolated polypeptide of the SARS virus.
2. The polypeptide of claim 1, wherein the polypeptide is a Spike (S) polypeptide, an Env (E) polypeptide, a Membrane (M) polypeptide, a hemagglutinin-esterase polypeptide (HE), a
5 nucleocapsid (N) polypeptide, a ORF1a polypeptide, a ORF1ab polypeptide, a proteolytic fragment of a ORF1a polypeptide, or a proteolytic fragment of a ORF1ab polypeptide.
3. The polypeptide of claim 1, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6039, 7232, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 6042, 6043, 6044, 6045, 6046, 6047,
10 6048, 6049, 6050 or 6052.
4. The polypeptide of claim 1, wherein the polypeptide comprises an amino acid sequence having >75% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6042, 6043, 6044, 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316,
15 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.
5. The polypeptide of claim 1, wherein the polypeptide comprises a fragment of at least 10 consecutive amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6042, 6043, 6044, 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769,
20 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316, 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11552, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.
6. A polypeptide comprising an amino acid sequence having >80% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO^s: 6042, 6043, 6044,
25 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316, 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11552, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.
7. A polypeptide comprising an amino acid sequence that comprises a fragment of at least
30 10 consecutive amino acids of an amino acid sequence selected from the group consisting SEQ ID NO^s: 6042, 6043, 6044, 6045, 6046, 6047, 6048, 6049, 6050, 6052, 9766, 9767, 9768, 9769, 9770, 9771, 9772, 9773, 9774, 9775, 9776, 9777, 9778, 9779, 9997, 9998, 10149, 10316, 10338, 10339, 10340, 10341, 10342, 10532, 10533, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 11552, 11561, 11562, 11618, 11619, 11620, 11627, 11630, 11633 & 11636.

8. A polypeptide comprising an amino acid sequence having >80% sequence identity to SEQ ID NO: 6042, and/or comprising an amino acid sequence that comprises a fragment of at least 10 consecutive amino acids of SEQ ID NO: 6042, wherein the polypeptide is in the form of a trimer.
- 5 9. Nucleic acid encoding the polypeptide of any one of claims 1 to 8.
10. Nucleic acid according to claim 9, comprising a nucleotide sequence selected from the group consisting of SEQ ID NO^S: 7191, 7273, 7275, 7277, 7279, 7281, 7283, 7285, 7287, 7289, 7291, 7292, 7293, 9968, 10066, 10084, 10299, 10505, 11323, 11563, 11639 & 11640.
- 10 11. A polynucleotide comprising a nucleotide sequence having >80% sequence identity to the nucleic acid of claim 9 or claim 10.
12. A polynucleotide comprising a fragment of at least 10 consecutive nucleotides of the nucleic acid of claim 9 or claim 10.
13. Antibody that recognizes the polypeptide of any one of claim 1 to 8.
14. The antibody of claim 13, wherein said antibody recognizes the polypeptide comprising
15 the amino acid sequence of SEQ ID NO: 6042 or a fragment thereof.
15. The antibody of claim 14, wherein said antibody recognizes the polypeptide comprising the amino acid sequence of SEQ ID NO: 6042 or a fragment thereof in trimeric form.
16. The antibody of claim 13, wherein the antibody is a monoclonal antibody,
17. The antibody of claim 13, wherein the antibody is a human antibody,
- 20 18. An immunoassay for detecting a SARS virus antigen in a sample, comprising the step of contacting the sample with the antibody of any one of claims 13 to 17.
19. An immunoassay for detecting an antibody against a SARS virus antigen in a sample, comprising the step of contacting the sample with the polypeptide of any one of claims 1 to 8.
- 25 20. A method of detecting an antibody against a SARS virus antigen in a sample comprising contacting said sample with the polypeptide of any one of claims 1 to 8, under conditions suitable for binding said polypeptide to said antibody, if present, and detecting the binding of said polypeptide to said antibody.
- 30 21. A method for detecting a SARS virus antigen in a sample comprising contacting said sample with the antibody of any one of claims 13 to 17, under conditions suitable for binding said antibody to said antigen, if present, and detecting the binding of said antibody to said antigen.

22. A vaccine for the treatment or prevention of severe acute respiratory syndrome (SARS), comprising an inactivated SARS virus, a killed SARS virus, an attenuated SARS virus, a split SARS virus preparation, or at least one purified SARS virus antigens.
23. The vaccine of claim 22, comprising a purified polypeptide according to any one of
5 claims 1 to 8.
24. The vaccine of claim 22 or claim 23, wherein the antigen is a purified SARS virus antigen in the form of a VLP.
25. The vaccine of any one of claims 22 to 24, further comprising an adjuvant.
26. The vaccine of claim 25, wherein the adjuvant is an aluminium salt or is MF59.
- 10 27. The vaccine of any one of claims 22 to 26, comprising more than one SARS virus antigen.
28. The vaccine of claim 27, wherein the antigens are selected from S, E, N and M.
29. The vaccine of claim 22, comprising an inactivated SARS virus.
30. The vaccine of claim 29, wherein said virus is inactivated by chemical or physical means.
- 15 31. The vaccine of claim 30, wherein said inactivation comprises treatment of the virus with an effective amount of one or more of the following agents selected from the group consisting of detergents, formaldehyde, formalin, β -propiolactone, and UV light.
32. The vaccine of claim 30, wherein said inactivation comprises treatment of the virus with an effective amount of one or more of the following agents selected from the group consisting of
20 methylene blue, psoralen and carboxyfullerene (C60).
33. The vaccine of claim 30, wherein said inactivation comprises treatment of the virus with an effective amount of one or more of the following agents selected from the group consisting of binary ethylamine, acetyl ethyleneimine and gamma irradiation.
34. The vaccine of claim 31, wherein said inactivation comprises treatment with β -
25 propiolactone.
35. The vaccine of claim 34, wherein said β -propiolactone is used at a concentration of 0.01 to 0.5%.
36. The vaccine of claim 34, wherein said β -propiolactone is used at a concentration of 0.5 to 0.2%.
- 30 37. The vaccine of claim 34, wherein said β -propiolactone is used at a concentration of 0.025 to 0.1%.

38. A method of inactivating SARS virus comprising exposing the virus to an inactivation agent for 12 to 24 hours at refrigeration temperatures followed hydrolysis of any residual inactivating agent by elevating the temperature for three hours.
39. The method of claim 38, wherein the inactivation agent is β -propiolactone.
- 5 40. The method of claim 38, wherein the refrigeration temperature is between 0°C and 8°C.
41. The method of claim 38, wherein the elevated temperature is between 33°C and 41°C.
42. A method for making an inactivated SARS vaccine comprising:
- a. innoculating a mammalian cell culture with SARS virus;
 - b. cultivating the infected cells;
 - 10 c. harvesting SARS virus containing supernatant;
 - d. inactivating the SARS virus; and
 - e. purifying the inactivated SARS virus.
43. The method of claim 42, wherein said mammalian cell culture is derived from one or more of the cell types selected from the group consisting of fibroblast cells, endothelial cells, 15 hepatocytes, keratinocytes, immune cells, mammary cells, smooth muscle cells, melanocyte cells, neural cells, prostate cells, renal cells, skeletal cells, liver cells, retinoblast cells and stromal cells.
44. The method of claim 42, wherein said mammalian cell culture is derived from a cell culture selected from the group consisting of human cells, non-human primate cells, HeLa cells, 20 human diploid cells, fetal rhesus lung cells, human embryonic kidney cells, VERO cells, horse cells, cow cells, sheep cells, dog cells, cat cells or rodent cells.
45. The method of claim 42, wherein said mammalian cell culture is derived from VERO cells or fetal rhesus kidney cells.
46. The method of claim 42, wherein said mammalian cells are cultured in serum free media.
- 25 47. The method of claim 42, wherein said mammalian cells are cultured in protein free media.
48. The method of claim 42, wherein said inoculating step comprising absorbing the SARS virus onto the cell culture for 60 to 300 minutes.
49. The method of claim 42, wherein said inoculating step is conducted at 25°C to 40°C.
- 30 50. The method of claim 42, wherein said purification step comprises one or more of the treatments selected from the group consisting of gradient centrifugation, ultracentrifugation, continuous-flow ultracentrifugation, chromatography, polyethylene glycol precipitation, and ammonium sulfate precipitation.

51. The method of claim 42, wherein said purification step comprises one or more of the treatments selected from the group consisting of ultrafiltration and dialfiltration.

52. The method of claim 50, wherein said chromatography treatment includes one or more of the chromatography treatments selected from the group consisting of ion exchange
5 chromatography, size exclusion chromatography, and liquid affinity chromatography.

53. The method of claim 52, wherein said chromatography treatment includes use of one more chromatographic resins selected from the group consisting of an anionic resin and a cationic resin.

54. The method of claim 52, wherein the ion exchange chromatography treatment includes a
10 first step using a strong anion exchange resin and a second step using a strong cation exchange resin.

55. The method of claim 50, wherein said gradient centrifugation purification step comprises density gradient centrifugation.

56. The method of claim 42, wherein said purification step comprises a first step of
15 chromatography purification and a second step of gradient centrifugation.

57. The method of claim 56, wherein said first chromatography purification step comprises liquid affinity chromatography.

58. The method of claim 56, wherein said second gradient centrifugation step comprises density gradient centrifugation.

59. A single-stranded oligonucleotide comprising a nucleotide sequence selected from the
20 group consisting of SEQ ID NOS: 21-6020, 6076-6568, 6586-6587, 7292-7301, 7325-7328, 7332-7352, 7353-7385, 10235-10298, 10352-10504, 10580-11322 and 11325-11551.

60. A single-stranded oligonucleotide comprising the complement of the oligonucleotide of claim 59.

25 61. The oligonucleotide of claim 59 or claim 60, comprising 10-30 nucleotides.

62. The oligonucleotide of claim 61, comprising the nucleotide sequence of SEQ ID NO: 7292, SEQ ID NO: 7293, the complement of SEQ ID NO: 7292 or the complement of SEQ ID NO: 7293.

63. A kit comprising primers for amplifying a template sequence contained within a SARS
30 virus nucleic acid target, the kit comprising a first primer and a second primer, wherein the first primer comprises a sequence substantially complementary to a portion of said template sequence and the second primer comprises a sequence substantially complementary to a portion of the

complement of said template sequence, wherein the sequences within said primers which have substantial complementarity define the termini of the template sequence to be amplified.

64. The kit of claim 63, wherein the template sequence is contained within SEQ ID NO: 1 and/or SEQ ID NO: 2.

5 65. The kit of claim 63 or claim 64, wherein the first primer comprises a fragment of 8 or more nucleotides of SEQ ID NO: 1, and the second primer comprises a fragment of 8 or more nucleotides of the complement of SEQ ID NO: 1.

66. The kit of claim 63 or claim 64, wherein the first primer comprises a fragment of 8 or more nucleotides of SEQ ID NO: 2, and the second primer comprises a fragment of 8 or more
10 nucleotides of the complement of SEQ ID NO: 2.

67. The kit of claim 63, wherein the first primer is an oligonucleotide according to any one of claims 59 to 62 and the second primer is an oligonucleotide according to any of claims 59 to 62.

68. The kit of any one of claims 63 to 67, further comprising a labeled probe that comprises either a fragment of 8 or more nucleotides of SEQ ID NO: 1 and/or SEQ ID NO: 2, or the
15 complement of said fragment, which fragment is located within the template sequence.

69. The kit of any one of claims 63 to 68, wherein the first primer and/or the second primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS: 21-6020, 6076-6568, 6586-6587, 7292-7301, 7325-7328, 7332-7352, 7353-7385, 10235-10298, 10352-10504, 10580-11322 and 11325-11551.

70. The kit of any one of claims 63 to 68, wherein the first primer and/or the second primer comprises the complement of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 21-6020, 6076-6568, 6586-6587, 7292-7301, 7325-7328, 7332-7352, 7353-7385, 10235-10298, 10352-10504, 10580-11322 and 11325-11551.

71. A method of detecting the presence of SARS virus in a sample comprising providing a
5 sample suspected of containing a SARS virus nucleic acid target, amplifying a template sequence contained within said SARS virus nucleic acid target with the kit of any one of claims 63 to 70, and detecting the amplified template sequence, wherein the presence of the amplified template sequence indicates the presence of SARS virus in said sample.

72. The method of claim 71, wherein said amplifying is accomplished using polymerase
0 chain reaction, transcription mediated amplification, reverse transcription PCR, ligase chain reaction, strand displacement amplification or nucleic acid sequence-based amplification.

73. A double-stranded RNA molecule with a length from about 10 to about 30 nucleotides which is able to inactivate the SARS coronavirus in a mammalian cell.

74. The double-stranded RNA of claim 73, wherein the sequence of one of the strands is at least 90% identical to a target sequence, wherein the target sequence is a fragment of SEQ ID NO: 1 and/or SEQ ID NO: 2.
75. The double-stranded RNA of claim 73 or claim 74, wherein the target sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 7292, 7293, 7294, 7295, 7296, 7297, 7298, 7299, 7300 and 7301.
76. The double-stranded RNA of any one of claims 73 to 75, comprising at least one modified nucleotide.
77. A method for treating a patient suffering from SARS, comprising: administering to the patient a therapeutically effective dose of a molecule of less than 1000 g/mol.
78. The method of claim 77, wherein the molecule has an aromatic region and greater than one heteroatom selected from O, S, or N.
79. A method for treating a patient suffering from SARS, comprising: administering to the patient a therapeutically effective dose of a compound selected from: a nucleoside analog, a peptoid, an oligopeptide, a polypeptide a protease inhibitor, a 3C-like protease inhibitor, a papain-like protease inhibitor, or an inhibitor of an RNA dependent RNA polymerase.
80. A method for treating a patient suffering from SARS, comprising: administering to the patient a steroidal anti-inflammatory drug in combination with at least one antiviral compound.
81. A method for treating a patient suffering from SARS, comprising: administering to the patient a therapeutically effective dose of a compound selected from: acyclovir, gancyclovir, vidarabidine, foscarnet, cidofovir, amantidine, ribavirin, trifluorothymidine, zidovudine, didanosine, zalcitabine, an antiviral compound listed in Table 1; an antiviral compound listed in Table 2; or an interferon.
82. The method of claim 81, wherein the interferon is an interferon- α or an interferon- β .
83. The method of any one of claims 77 to 82, wherein the molecule or compound is delivered by inhalation.
84. A method of identifying a therapeutically active agent comprising the steps of: (a) contacting a therapeutically active agent with a cell infected with the SARS virus; (b) measuring attenuation of a SARS related enzyme.
85. A viral vector or particle for *in vivo* delivery of a nucleic acid of claim 9 or claim 10.
86. The viral vector of claim 85, wherein the vector is an adenovirus vector, a poxvirus vector or an alphavirus vector.
87. An alphavirus replicon particle comprising one or more SARS viral antigens.

88. The replicon particle of claim 87, wherein said SARS viral antigen is a spike protein.
89. The replicon particle of claim 87, wherein said particle comprises a replicon derived from Venezuelan Equine Encephalitis (VEE) and further comprises an envelope derived from Sindbus virus (SIN) or Semliki Forest Virus (SFV).
- 5 90. A vaccine comprising one or more SARS virus antigens and one or more respiratory virus antigens.
91. The vaccine of claim 90, wherein said respiratory virus antigens are selected from the group consisting of influenza virus, human rhinovirus (HRV), parainfluenza virus (PIV), respiratory syncytial virus (RSV), adenovirus, metapneumovirus, and rhinovirus.
- 10 92. The vaccine of claim 91, wherein said respiratory virus antigen is from influenza virus.
93. The vaccine of claim 90, wherein said respiratory virus antigen is from a coronavirus other than the SARS virus.
94. A polypeptide comprising an immunogenic, surface exposed fragment of the amino acid sequence SEQ ID NO: 6042.
- 15 95. The polypeptide of claim 94, wherein said fragment does not include the last 50 amino acids of the C-terminus of SEQ ID NO: 6042.
96. The polypeptide of claim 94, wherein said fragment does not include a transdomain region of SEQ ID NO: 6042.
97. The polypeptide of claim 94, wherein said fragment does not include a C-terminus
20 cytoplasmic domain of SEQ ID NO: 6042.
98. The polypeptide of claim 94, wherein said fragment does not include a N-terminus signal sequence.
99. An isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 9968 and 10066.
- 25 100. The polynucleotide of claim 99, wherein the polynucleotide comprising a nucleic acid sequence having > 80% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 9968 and 10066.
101. An isolated polynucleotide comprising a fragment of at least 15 consecutive nucleic acids of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 9968 and 10066
30 and wherein said fragment does not consist entirely of SEQ ID NO: 10033.
102. An isolated polypeptide comprising an amino acid sequence encoded by any one of claims 99 – 101.

103. The polypeptide of claim 102, comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 9969 – 10032, 10067, and 10015.
104. The polypeptide of claim 103, wherein the amino acid sequence is selected from the group consisting of SEQ ID NOS: 9997, 9998 and 10015.
- 5 105. An expression construct for recombinant expression of a SARS virus spike protein wherein said construct comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 6578 – 6583.
106. A mammalian cell line stably expressing a SARS viral antigen.
107. The cell line of claim 106, wherein said cell line is a Chinese Hamster Ovary (CHO) cell.
- 10 108. The cell line of claim 106, wherein the SARS viral antigen is a spike protein or fragment thereof.
109. The cell line of claim 106, wherein the spike protein is truncated to remove the transmembrane sequence.
110. A method of identifying a therapeutically active agent comprising the steps of: (a)
- 15 contacting a therapeutically active agent with a buffer comprising SARS enzyme; and (b) measuring attenuation of the SARS enzyme.
111. The method of claim 110 wherein the SARS enzyme is a SARS protease.
112. The method of claim 111 wherein the buffer further comprises a peptide with a SARS protease cleave site.
- 20 113. The method of claim 110 wherein the measurement is made by the measurement of fluorescence.
114. A vaccine of one of claims 22 to 37, and 90 to 93 further comprising an adjuvant.
115. The vaccine of claim 114 wherein the adjuvant is a SMIP.
116. The vaccine of claim 115 wherein the SMIP compound is selected from the group
- 25 consisting of an acylpiperazine, a tryptanthrin, an indoleione, a tetrahydroisoquinoline, a benzocyclodione, an amino azavinyl compound, a thiosemicarbazone, a lactam, an aminobenzimidazole quinolinone, a hydrophthalamide, a benzophenone, an isoxazole, a sterol, a quinazolinone, a pyrole, an anthraquinone, a quinoxaline, a triazine, an benzazole, and a pyrazolopyrimidine, or a pharmaceutically acceptable salt, ester, or prodrug thereof.
- 30 117. A method of vaccinating a subject comprising administering a vaccine of one of claims 22 to 37, and 90 to 93.
118. The method of claim 117 further comprising administering a SMIP.

119. A method for treating a patient of one of claims 77 to 82 further comprising administering at least one SMIP compound.

120. A method for treating a patient of one of claims 77 to 82 further comprising administering at least one SMIS compound.

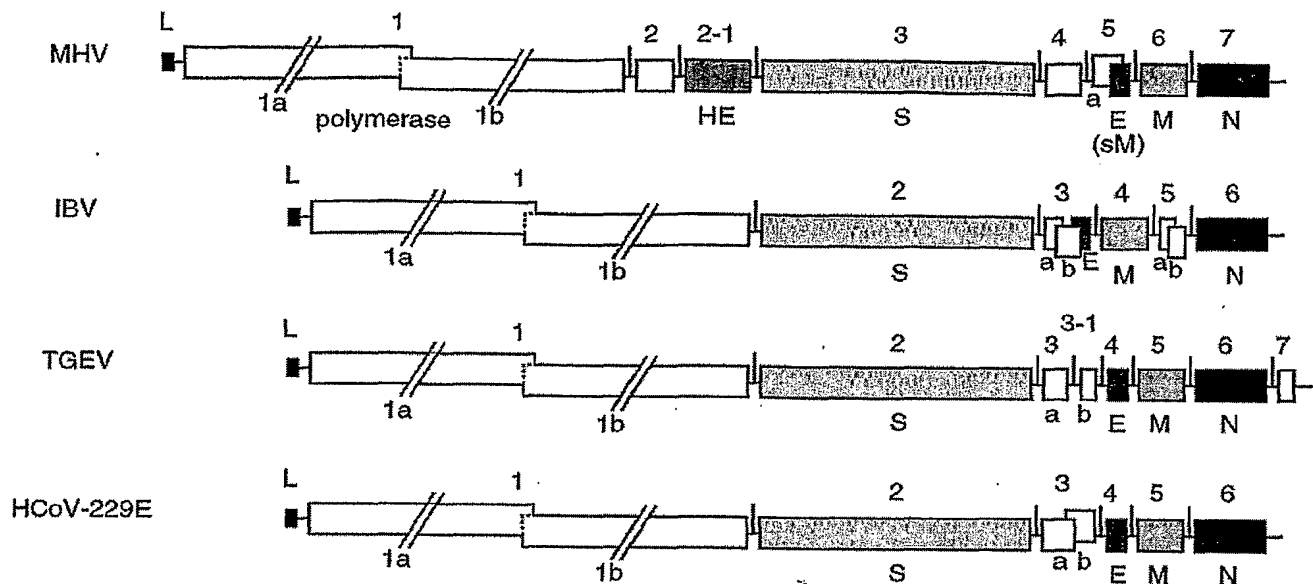
FIGURE 1

FIGURE 2

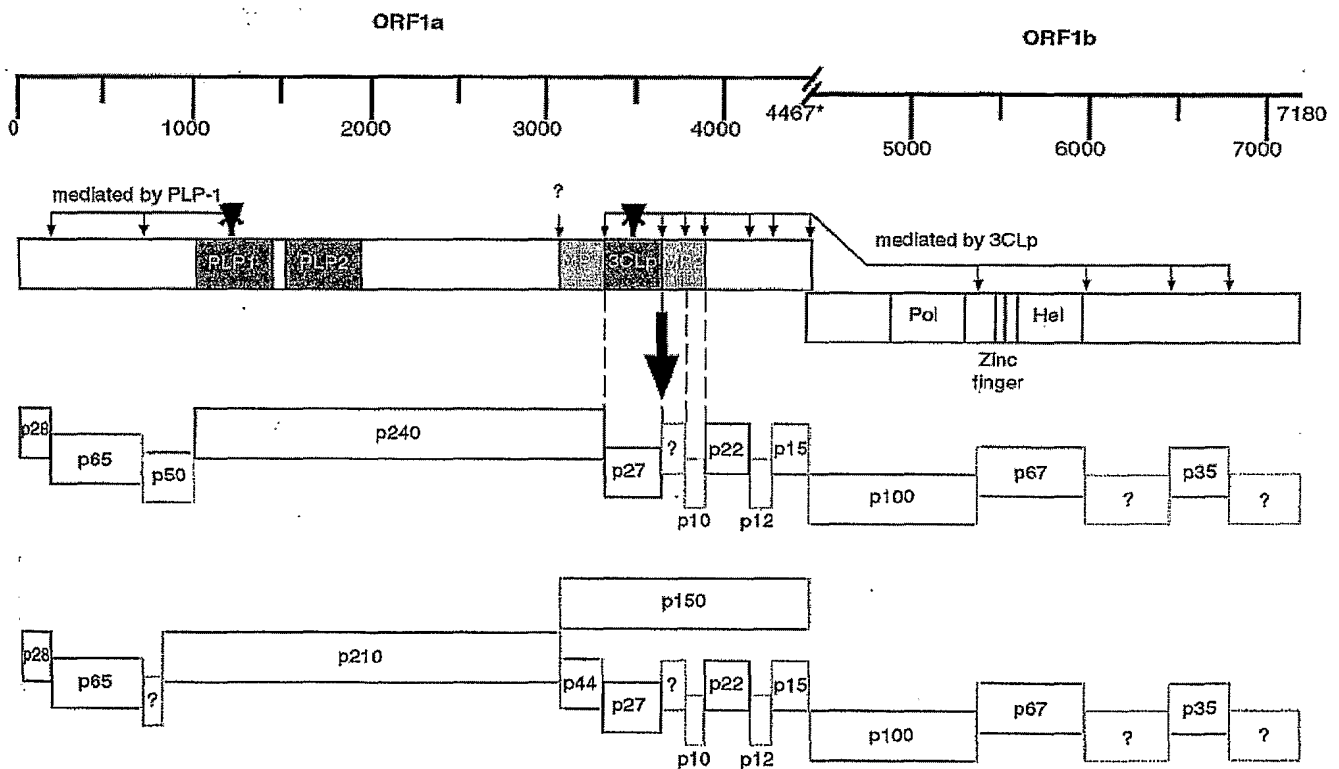


FIGURE 3**FIGURE 3A**

		Section 1				
		(1) 1	10	20	30	43
BCV N	(1)	ATGTCCTTTT	ACTCCTGGT	-AAGCAAT	-CCAGTAGTAGAGCGT	
MHV N	(1)	ATGTCCTTTT	GTTCTGGGG	CAAGAAAAT	GCCGGTGGCAGAAAGCT	
Avian infectious bronchitis N	(1)	-----	-----	-----	-----	-----
Consensus	(1)	ATGTCCTTTT	TCCTGG	AAG AA	CC GT G AGA	T
		Section 2				
		(44) 44	50	60	70	86
BCV N	(41)	CGTTTGGAAT	CGTTCTGGTAAT	TGGCATCCTTAAG	-----	-----
MHV N	(44)	CCTCTGTAAACCG	CGCTGGTAAT	TGGAATCCTCAAGAAGACCAC		
Avian infectious bronchitis N	(1)	-----	-----	-----	-----	-----
Consensus	(44)	CCT TG AAA CG	CTGGTAATGG	ATCCT AAG		
		Section 3				
		(87) 87	100	110		129
BCV N	(76)	-TGGGCGGATCAGT	CCGACCAATCTAGAAAT	GTTCAAACCAGG		
MHV N	(87)	TTGGGGCTGACCAAAC	CGAGCGTGGACCAAATAAT	CAAAATAGA		
Avian infectious bronchitis N	(1)	-----	-----	-----	-----	-----
Consensus	(87)	TGGGC GA CA	CCGAGCG T AAGAAAT	TCAA CAGA		
		Section 4				
		(130) 130	140	150	160	172
BCV N	(118)	GGTAGAAGAGCTCA	ACCCCAAGGAAACTG	GCTACTTCTCAGCTAC		
MHV N	(130)	GGCAGAAGGAATCAG	CCAAGCAGACTGCAACT	ACTCAAC--C		
Avian infectious bronchitis N	(33)	CTCCCCCGCGCCAATC	---ATCAAACTAGGAGGACCAAAA--C			
Consensus	(130)	GGCAGAAG GCTCA CC	AAGCAAACTGC ACTACTCAAC	C		
		Section 5				
		(173) 173	180	190	200	215
BCV N	(161)	CATCAGGAGGGAATG	TGTGTACCCCTACTAT	-TCTTGCTTCTCTG		
MHV N	(171)	CAACTCC-GGGAGTGT	GGTTCCCCATTAC	-TCCTGGTTTCTGTG		
Avian infectious bronchitis N	(71)	CACCAAA-GGTAGGGT	CATCTGGAAATGCATCT	TGGTTTCAAG		
Consensus	(173)	CA CA	GGGAGTGT GT CCC A TAC	TCTTGGTTTTCTG		
		Section 6				
		(216) 216	230	240		258
BCV N	(203)	GAATTAA---CTCAGTTT	CAAAAAGGAAAGGAGTTT	GAATTTGC		
MHV N	(212)	GCATTAA---CCCACTT	CAAAAAGGAAAGGAGTTT	CAGTTTGC		
Avian infectious bronchitis N	(113)	CCATAAAGGCCAA	GAACTAAATGCACCTGCACCTAAGTTTG-			
Consensus	(216)	GCATTAA	CCCAGTT CAAAA GGAAAGGAGTTT	AGTTTGC		
		Section 7				
		(259) 259	270	280	290	301
BCV N	(243)	AGAGGGACAAGGTGT	GCCTATTGCAACAGGAGTCCCAGCTACT			
MHV N	(252)	AGAAGGACAAGGAGT	GCCTATTGCCAATGGAATCCCCGCTTCA			
Avian infectious bronchitis N	(155)	--AAGGTAGTGCTGT	TCTGTATTAATGAAAATCTTAAAAATAGC			
Consensus	(259)	AGAAGGACAAGGTGT	GCCTATTGC AAGGA TCCCAGCTAC			

FIGURE 3A (contd.)

						Section 8
	(302)	302	310	320	330	344
BCV N	(286)	GAAGCTAAGGGGTACTGGTACAGACACAACAGACGTTCTTTTA				
MHV N	(295)	GAGGAAAAGGGATATTGGTATAGACACAACCGCCGTTCTTTTA				
Avian infectious bronchitis N	(196)	CAGCAGCACGGGTACTGGAGGCGCCAAGCCAG-----GTTTA				
Consensus	(302)	GAGCA AAGGGGTACTGGTA AGACACAACAG CGTTCTTTTA				
						Section 9
	(345)	345	350	360	370	387
BCV N	(329)	AAACAGCCGATGGCA-ACCAGCGTCAACTGCTGCCACCGATGGT				
MHV N	(338)	AAACACCTGATGGGC-AGCAGAGCAATTACTGCCCAGATGGT				
Avian infectious bronchitis N	(233)	AGCCAGGTAAAGGCGGAAGAAAACCAAGTCCCTGATGCC-TGGT				
Consensus	(345)	AAACAGCTGATGGC A CAGAA CAATT CTGCC CGATGGT				
						Section 10
	(388)	388	400	410	420	430
BCV N	(371)	ATTTTACTATCTTGGAAACAGGACCGCATGCCAAGACCAGTA				
MHV N	(380)	ATTTTACTATCTTGGCACAGGGGCCCATGCTGGAGCCAGTTA				
Avian infectious bronchitis N	(275)	ATTTCTATTACACTGGAACAGGACCAGCCGCTGACCTGAATTG				
Consensus	(388)	ATTTTACTATCTTGGAAACAGGACC CATGCTGAAG CAATTA				
						Section 11
	(431)	431	440	450	460	473
BCV N	(414)	TGGCACCGATATTGACGGAGTCTTCTGGGTGCTAGTAACCAG				
MHV N	(423)	TGGAGACAGCATTGAACGTGTCTTCTGGGTGCAAAACAGCCAA				
Avian infectious bronchitis N	(318)	GGGTGATTCTCAAGATGGTATAGTGTGGGTTGCTGCTAAGGGT				
Consensus	(431)	TGG GAC TATTGA GGTGTCTTCTGGGTTGCTA TAACCA				
						Section 12
	(474)	474	480	490	500	516
BCV N	(457)	GCTGATGTCAATACCCCGGCTGACATTCTCGATCGGGAGCCCAA				
MHV N	(466)	GCGGACACCAATACCCGCTCTGATATTGTGAAAGGGAGCCCAA				
Avian infectious bronchitis N	(361)	GCTGATGTGAAATCTAGATCCAACAGGGTACTAGAGATCCTG				
Consensus	(474)	GCTGATGTCAATACCCG TCTGACATTGTGATAGGGAGCCCAA				
						Section 13
	(517)	517	530	540		559
BCV N	(500)	GTAGCGATGAGGCTATTCCGACTA-GGTTTCGGCCTGGCACGG				
MHV N	(509)	GCAGTCATGAGGCTATTCCACTA-GGTTTGCGCCCGGCACGG				
Avian infectious bronchitis N	(404)	ATAAGTTTGAT-CAATACCCACTACGGTTTTCAGATGG-----				
Consensus	(517)	GTAG ATGAGGCTATTCC ACTA GGTTT CGCCTGGCACGG				
						Section 14
	(560)	560	570	580	590	602
BCV N	(542)	TACTCCCTCAGGGTTACTATATTGAAGGCTCAGGAAGGTCTGC				
MHV N	(551)	TATTGCCTCAGGGCTTTTATGTTGAAGGCTCTGGAAGGTCTGC				
Avian infectious bronchitis N	(441)	-AGGACCTGATGGTAATT-----TCCGTTGGGACTTC				
Consensus	(560)	TA T CCTCAGGGTTATTAT TTGAAGGCTC GGAAGGTCTGC				

FIGURE 3A (contd.)

Section 15

	(603)	603	610	620	630	645
BCV N	(585)	TCCTAATTCAGATCTACTTCACGCGCA	---TCCAGTAGAGCC			
MHV N	(594)	ACCTGCTAGCCGATCTGGTTCGCGGT	CACAATCCCGTGG-GCC			
Avian infectious bronchitis N	(472)	AT-TCCCTCTGAGTCGTGGTAGGAGTGG	AAGATCAACCCGAGCA			
Consensus	(603)	ACCT CT CAGATCTGGTTCGCG	GCA ATCCAGTGGAGCC			

Section 16

	(646)	646	660	670	688
BCV N	(625)	TCAGTGCAGGATCGCGTAGTAGAGCCA	ATTCTGGCAACAGAA		
MHV N	(636)	AAATA-----ATCGCG--CTAGAAG	CAGTTCCAACCCGCGCC		
Avian infectious bronchitis N	(514)	TCATCAGCGGCATCTAG---	TAGAGTACCAATCCCGTGAGGGTT		
Consensus	(646)	TCAT GC G ATCGCG	TAGAG CA TTCC GC AG G		

Section 17

	(689)	689	700	710	720	731
BCV N	(668)	CCCCACCTCTGGTGTAACACCTGATAT	GGCTGATCAAATTGC			
MHV N	(671)	AGCCCTGCTCTACTGTAAACCTGATAT	GGCCGAAGAAATTGC			
Avian infectious bronchitis N	(554)	CACGTGGTCGTAGGAGTGGAGCTGA---	AGATGATCTGATTGC			
Consensus	(689)	C CCTGCCTCTAGTGTAACCTGATAT	GGCTGATCAAATTGC			

Section 18

	(732)	732	740	750	760	774
BCV N	(711)	TAGTCTTGTTCTGGCAAAACCTTGGCA	AAGGATCCCACTAAGCCA			
MHV N	(714)	TGCTCTTGTTTGGCTAAGCTCGGTAA	AGATGCCGGCCAGCCC			
Avian infectious bronchitis N	(594)	CCGTGCAGCAAAGATTATTACGACCAG	CAG---AGGAAGGGT			
Consensus	(732)	T GTCTTGTT TGGCTAA CT GGCA	AAGGATGCCAG AAGCC			

Section 19

	(775)	775	780	790	800	817
BCV N	(754)	CAGCAAGTAACCTAAGCAGACTGCCAA	AAGAAATCAGACA--GAA			
MHV N	(757)	AAGCAAGTAACGAAGCAAAGTGCCAA	AGAAGTCAGGCA--GAA			
Avian infectious bronchitis N	(634)	ACGCGCATTACTAAGCAAAAGGCAGA	AAGAGATGGCTCATCCCC			
Consensus	(775)	AAGCAAGTAACCTAAGCAAA TGCCA	AAGAAATCAG CA GAA			

Section 20

	(818)	818	830	840	850	860
BCV N	(795)	AATTTTGAATAAGCCCCGCCAGAGAG	AGCCCCAATAAACA			
MHV N	(798)	AATTTTAAACAAGCCTCGCCAAAAGAG	GACTCCAAACAAGCAG			
Avian infectious bronchitis N	(677)	GATTCGTGAAGCGTACGGTGCCACCAG	GTTATAGAGTAGATCA			
Consensus	(818)	AATTTTGA AAGCCCCGCCA AAGAGGA	CC AATAAACA			

Section 21

	(861)	861	870	880	890	903
BCV N	(838)	TGCACGTTCAGCAGTGTTTTGGGAAG	AGAGGCCCAATCAGA			
MHV N	(841)	TGCCCAGTGCAGCAGTGTTTTGGAAAG	AGAGGCCCAATCAGA			
Avian Infectious bronchitis N	(720)	AGTTTTTGGCCCTCGTACTAAAGGTAA	AGGGT-----A			
Consensus	(861)	TGC CTGTGCAGCAGTGTTTTGGGAAG	AGAGGCCCAATCAGA			

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FIGURE 3A (contd.)

Section 22

	(904)	904	910	920	930	946
BCV N	(881)	ATTTTGGTGGTGGAGAAATGTTAAAACTTGGAACTAGTGACCC				
MHV N	(884)	ATTTTGGAGGCTCTGAAATGTTAAAACTTGGAACTAGTGATCC				
Avian infectious bronchitis N	(755)	ATTTTGGTGTATGACAAGATGAATGAGGAAGGTATTAAGGATGG				
Consensus	(904)	ATTTTGGTGGTG	GAAATGTTAAAACTTGGAACTAGTGATCC			

Section 23

	(947)	947	960	970	989
BCV N	(924)	ACAGTTCCCCATTCTTGCGAGAAC	-TCGCACCCACAGCTGGTGCC		
MHV N	(927)	ACAGTTCCCCATTCTTGCGAGAGT	-TGGGTCCAACAGTTGGTGCC		
Avian infectious bronchitis N	(798)	GC-GTGTACAGCAATGCTCAACCTTACACCAAGCCGACATGC			
Consensus	(947)	ACAGTTCCCCATTCTTGCGAGAAC	TGCACCAACAGCTGGTGCC		

Section 24

	(990)	990	1000	1010	1020	1032
BCV N	(966)	GTTTTCTTTGGATCAAGATTAGAGTTGGCCAAAGTGCAGAAT				
MHV N	(969)	CTTCTTCTTTGGATCTAAATTAGAATTGGTCAAAA	---AGAAT			
Avian infectious bronchitis N	(840)	TGTCTTTTGGAGTAGAGT-GAC	---GCCCCAAG	-----		
Consensus	(990)	TTTTTCTTTGGATCTAGATTAGA	TTGGCCAAAG	AGAAT		

Section 25

	(1033)	1033	1040	1050	1060	1075
BCV N	(1009)	TTGTCTGGGAATCTTGACGAGCCCCAGAGGATGTTTATGAAT				
MHV N	(1009)	T---CTGGTGGTGGCTGATGAACCCACCAAGATGTGTATGAGC				
Avian infectious bronchitis N	(871)	----CT--TCACACAGATGGGCTTC	---ACCTTAGATTGGAAT			
Consensus	(1033)	TCTGGTATCCTGATGAGCCCC	AA	GATGT	TATGAAT	

Section 26

	(1076)	1076	1090	1100	1118
BCV N	(1052)	TGCGCTATAATGGTGCAATTAGATTTGACAGTACACTTTTCAGG			
MHV N	(1049)	TGCAATATTCAGGTGCAGTTAGATTTGATAGTACTCTACCTGC			
Avian infectious bronchitis N	(905)	TT-ACTACTGGGTGCC	--TAGAGATGACCCGCAAGTTTGATAA		
Consensus	(1076)	TGCACTATT	TGGTGCA	TTAGATTTGACAGTAC	CTTCTGG

Section 27

	(1119)	1119	1130	1140	1150	1161
BCV N	(1095)	TTTTGAGACCATA	----ATGAAGGTGTTGAATGAGAATTTGAA			
MHV N	(1092)	TTTTGAGACTATC	----ATGAAAGTGTGGAATGAGAATTTGAA			
Avian infectious bronchitis N	(945)	TTATGTAAAAATTTGTGATGAGTGTGTTGATGCTGTAG	--GAA			
Consensus	(1119)	TTTTGAGAC	AT	ATGAA	GTGTTGAATGAGAATTTGAA	

Section 28

	(1162)	1162	1170	1180	1190	1204
BCV N (1134)		TG	CATATCAACAACAAGATGGTAT	-GATGAATATGA	-GTCCAA	
MHV N (1131)		TG	CTACCAGAAGGATGGTGGTGCAGATGTGG	-TGA	-GCCCAA	
Avian infectious bronchitis N (986)		CAC	GTCCAAAGGACGAAGTTGTAA	-GACCAAAGT	CACGCCCAA	
Consensus (1162)		TGC	TACCAA	AACAAGGTGGTA	GATGAA	TGA GCCCAA

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FIGURE 3A (contd.)

Section 29					
	(1205)	1205	1210	1220	1230
BCV N (1175)		AACCACAGCGTCA	---	GCGTGGTCAG	---
MHV N (1172)		AGCCCCAAAGAAAAGGGCGTAGACAGGCTCAGGAAAAGA	---	AAG	
Avian infectious bronchitis N (1028)		ATTCAAGACCTGC	---	TACAAGAAACAAG	---
Consensus (1205)		A CCACAACGT A		GCGTGGACAGG T A GAA	GACAAG
Section 30					
	(1248)	1248	1260	1270	1280
BCV N (1211)		GAGAAAATGATAATATAAGTGTTCAGCGCCTAAAAGCCGTGT			
MHV N (1214)		ATGAAGTAGATAATGTAAGCGTTGCAAAGCCCAAAAGCTCTGT			
Avian infectious bronchitis N (1068)		ACAACAGCGTCAAAAGAAAGGAGAAGAGTCAAAGAAGCAGGAT			
Consensus (1248)		A GAAA	GATAATATAAG GTTGCAA GCC	AAAAGC GTGT	
Section 31					
	(1291)	1291	1300	1310	1320
BCV N (1254)		GCAGCAAAATAAGAGTAGAGAGTTGACTGCAGA	---	GGACATC	
MHV N (1257)		GCAGCGAAATGTAAGTAGAGAATTACCCAGA	---	GGATAGA	
Avian infectious bronchitis N (1111)		GATGAAGTAGATAAG	---	GCATTGACCTGAGATGAGGAGAGG	
Consensus (1291)		GCAGCAAAATATAAGTAGAGAATTGACC CAGA		GGA AG	
Section 32					
	(1334)	1334	1340	1350	1360
BCV N (1294)		AGCCTTCT	---	TAACAAGATGGATGA	---
MHV N (1297)		AGTCTGTTGGCTCAGATCCTTGATGATGGCGTAGTGCCAGATG			
Avian infectious bronchitis N (1150)		AACAATGCACAGCTGGAATTTGATGATGAACCCAAGGTGATTA			
Consensus (1334)		AGCCTT T	TCAGAA TTGATGATG		GCC ATA
Section 33					
	(1377)	1377	1390	1400	1414
BCV N (1325)		CT	---	GAAGACACCTCAGAAATATAA	---
MHV N (1340)		GGTTAGAAGATGACTCTAATGTGTAA	---		
Avian infectious bronchitis N (1193)		ACTGGGGGGATTTCAGCACTTGGAGAGAATGAGTTGTAA			
Consensus (1377)		T	GAAGAT CCTCA ATGTATAA		
BCV N		SEQ ID NO: 9883			
MHV N		SEQ ID NO: 9894			
Avian infectious bronchitis N		SEQ ID NO: 9903			

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FIGURE 3B

		Section 1				
		(1)	1	10	20	30 41
HOBMPRO	(1)	GATGTGGATGACGTTTAGGTAATCCAAACATTATGAGTAGT				
BCV M	(1)	-----ATGAGTAGT				
MHV M	(1)	-----ATGACTAGT				
Avian infectious brochitis virus M	(1)	-----				
Consensus	(1)	ATGAGTAGT				
		Section 2				
		(42)	42	50	60	70 82
HOBMPRO	(42)	AAAACCTA---CTCCAGCACCCAGTTTATATCTGGACTGCTGA				
BCV M	(10)	GTAACCTA---CACCAGCACCCAGTTTACACCTGGACTGCTGA				
MHV M	(10)	ACCACTCAGGCTCCACAGCCTGTTTATCAGTGGACGGCTGA				
Avian infectious brochitis virus M	(1)	--ATGTC---GAACGCGGCAAATTGCACCTCTGACTG-TGA				
Consensus	(42)	A AACTC CTCCAGCGCCAGTTTATCTCTGGACTGCTGA				
		Section 3				
		(83)	83	90	100	110 123
HOBMPRO	(80)	TGAAGCTATTAAATTCCTAAAGGAATGGAATTTTCTTTGG				
BCV M	(48)	TGAAGCTATTAAATTCCTAAAGGAATGGAACITTTCTTTGG				
MHV M	(51)	TGAGGCAATTCGATTCCCTTAAGGAATGGAATTTCTCTCTCG				
Avian infectious brochitis virus M	(36)	ACAGTCAGTTGAGCTTTTAAAGAAATATAATTTATTATATAA				
Consensus	(83)	TGAGGCTATTAAATTCCTTAAGGAATGGAATTTTCTTTGG				
		Section 4				
		(124)	124	130	140	150 164
HOBMPRO	(121)	GTATTATACTACTTTTTATTACAATCATATTGCAATTTGGA				
BCV M	(89)	GTATTATACTACTTTTTATTACAATCATATTGCAATTTGGA				
MHV M	(92)	GCATTATACTACTTTTTGTTACTATCATACTACAGTTCCGT				
Avian infectious brochitis virus M	(77)	CCGCATTCCCTATTGTTTCTTACTATACTACTTCAGTATGGA				
Consensus	(124)	GTATTATACTACTTTTTATTACTATCATATTGCAGTTTGA				
		Section 5				
		(165)	165	170	180	190 205
HOBMPRO	(162)	TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAGATGAT				
BCV M	(130)	TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAGATGAT				
MHV M	(133)	TACACGAGCCGTAGCATGTTTGTTTATGTTTGGAATGAT				
Avian infectious brochitis virus M	(118)	TATGCAACAAGGAGTCGGTTTATTACATAATGAAAATGAT				
Consensus	(165)	TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAGATGAT				
		Section 6				
		(206)	206	220	230	246
HOBMPRO	(203)	TATTTTGTGGCTTATGTGGCCCCCTTACTATAATCTTAACCTA				
BCV M	(171)	CATTTTGTGGCTTATGTGGCCCCCTTACTATCATCTTAACCTA				
MHV M	(174)	ACTTTTGTGGCTTATGTGGCCACTAACTATTGTTTGTGTA				
Avian infectious brochitis virus M	(159)	AGTGTTATCGTGCTTTTGGCCCCCTTAACATTGCAGTAGGTTG				
Consensus	(206)	AATTTTGTGGCTTATGTGGCCCCCTTACTATTGTCTTAAGTA				

FIGURE 3B (contd.)

Section 7						
	(247)	247	260	270	287	
HOBMPRO (244)	TTTTCAATTGCGTATACGCATTGAATAATGTGTATCTTGGC					
BCV M (212)	TTTTCAATTGCGTGTATGCGTTGAATAATGTGTATCTTGGC					
MHV M (215)	TTTTTAAC TGCGTCTATGCGCTAAATAATGTGTATCTTGGA					
Avian infectious brochitis virus M (200)	TAATTTCA TGTATATATCCACCAAATACAGGAGGTCTTGTCTC					
Consensus (247)	TTTTTAATTGCGTATATGCGTTGAATAATGTGTATCTTGGC					
Section 8						
	(288)	288	300	310	328	
HOBMPRO (285)	CTTTCCTATAGTTTTTACCATAGTGGCCATTATTATGTGGAT					
BCV M (253)	TTTTCTATAGTTTTCAC TATAGTGGCCATTATCATGTGGAT					
MHV M (256)	TTTTCTATAGTGTTTTACTATAGTGTCCATTATAATGTGGAT					
Avian infectious brochitis virus M (241)	GCAGCGAAAATACTTACAGTGGTTGCGTGTCTGTCTTTTGA					
Consensus (288)	TTTTCTATAGTTTTTACTATAGTGGCCATTAT ATGTGGAT					
Section 9						
	(329)	329	340	350	369	
HOBMPRO (326)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAACTG					
BCV M (294)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAACTG					
MHV M (297)	TATGTATTTTGTGAATAGCATCAGGTTGTTTATCAGGACTG					
Avian infectious brochitis virus M (282)	AGGATATTGGATTTCAGAGTATCAGACTCTTTAAGCGGGGTG					
Consensus (329)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGGACTG					
Section 10						
	(370)	370	380	390	400	410
HOBMPRO (367)	GAAGTTTTTGGAGTTTCAACCCAGAAACAAACAACCTTGATG					
BCV M (335)	GAAGTTGGTGGAGTTTCAACCCAGAAACAAACAACCTTGATG					
MHV M (338)	GCAGCTGGTGGAGCTTCAACCCGAAACAAACAACCTAATG					
Avian infectious brochitis virus M (323)	GGCAATGGTGGGCATTTAACCOCTGAGTCTAA-----TGCCG					
Consensus (370)	GAAGTTGGTGGAGTTTCAACCCAGAAACAAACAACCTTGATG					
Section 11						
	(411)	411	420	430	440	451
HOBMPRO (408)	TGTATAGATATGAAAGGAACAATGTATGTTAGGCCGATAAT					
BCV M (376)	TGTATAGATATGAAAGGGAAGGATGTATGTTAGGCCGATAAT					
MHV M (379)	TGTATAGATATGAAAGGTACTGTGTATGTTAGACCCATTAT					
Avian infectious brochitis virus M (359)	T-----AGGT-TCAATACTCCTATCTA-----ATGGTCAACAAT					
Consensus (411)	TGTATAGATATGAAAGGTACTATGTATGTTAGGCCGATAAT					
Section 12						
	(452)	452	460	470	480	492
HOBMPRO (449)	TGAGGACTATCATACTCTGACGGTCACAATAATACGCGGCC					
BCV M (417)	TGAGGACTAGCATACCCCTTACGGTCACAATAATACGTGGTC					
MHV M (420)	AGAGGATTACCATACTAACAGCCACTATCATTCGTGGTCTC					
Avian infectious brochitis virus M (392)	GTAATTTTGTCTATAGA--GAGTGTGCCAAT-----GGTG					
Consensus (452)	TGAGGATTACCATACTGACGGTCACAATAATACGTGGTCTC					

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FIGURE 3B (contd.)

						Section 13
	(493)	493	500	510	520	533
HOBMPRO (490)		ATGTTTACATTCAAGGTATAAACTAGGTACTGGCTATTCT				
BCV M (458)		ATCTTTACATGCAAGGTATAAACTAGGTACTGGCTATTCT				
MHV M (461)		ACCTCTATATGCAAGGTGTTAAGCTAGGCACCTGGCTTCTCT				
Avian infectious brochitis virus M (424)		CTTTCT - - - - CCAATTATAAAGAATGGAGTTCTTTATTGT				
Consensus (493)		ATCTTTACATGCAAGGTATAAAGCTAGGTACTGGCTATTCT				
						Section 14
	(534)	534	540	550	560	574
HOBMPRO (531)		TGGGCAGATTTGCCAGCTTATATGACTGTTGCTAAGGTTAC				
BCV M (499)		TTGTCAGATTTGCCAGCTTATGTGACTGTTGCTAAGGTTCTC				
MHV M (502)		TTGTCCTGATTTGCCCTGCTTATGTTACAGTTGCTAAGGTTGTC				
Avian infectious brochitis virus M (460)		GAGGGTCAGTGGCTTGC - - - - TAAATGTGAACCAGACCAC				
Consensus (534)		TTGTCCTGATTTGCCCTGCTTATGTGACTGTTGCTAAGGTTCTC				
						Section 15
	(575)	575	580	590	600	615
HOBMPRO (572)		ACACCTGTGCACATATAAGCGTGGTTTTCTTGACAGGATAA				
BCV M (540)		ACACCTGTCTCAGTATAAGCGTGGTTTTCTTGACAAGATAG				
MHV M (543)		TCACCTTTTGCACTTATAAGCGCGCATTCCTTAGACAAGGTAG				
Avian infectious brochitis virus M (496)		TTGCCATAAAGACATATTTG - - - - - TTTGCCCAACCAGATAG				
Consensus (575)		TCACCTGTGCACATATAAGCGTGGTTTTCTTGACAAGATAG				
						Section 16
	(616)	616	630	640		656
HOBMPRO (613)		GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
BCV M (581)		GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
MHV M (584)		ACGGTGTTAGCGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
Avian infectious brochitis virus M (531)		ACG-TAATA - - - - - TCTACCGTATG-GTGCAG - - - AAATA				
Consensus (616)		GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
						Section 17
	(657)	657	670	680		697
HOBMPRO (654)		GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCTGGCAT				
BCV M (622)		GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCTGGCAT				
MHV M (625)		GGAAATTACCGACTGCCCTCAAATAAACCGAGT - - - GGCAT				
Avian infectious brochitis virus M (562)		ACTGGTGACC-AAAGCGGAAATAAGAAAAGGTTTGCTACA-				
Consensus (657)		GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCTGGCAT				
						Section 18
	(698)	698	710	720		738
HOBMPRO (695)		GGACACCGCATTGTTGAGAAATAATATCTAAATTTTAAGGA				
BCV M (663)		GGACACCGCATTGTTGAGAAATAATATCTAA - - - - -				
MHV M (663)		GGACACCGCATTGTTGAGA - - - - - ATCTAA - - - - -				
Avian infectious brochitis virus M (601)		- - - - -				
Consensus (698)		GGACACCGCATTGTTGAGAAATAATATCTAA				
						Section 19
	(739)					
HOBMPRO (736)	TG	SEQ ID NO: 9912				
BCV M (694)	--	SEQ ID NO: 9884				
MHV M (688)	--	SEQ ID NO: 9895				
Avian infectious brochitis virus M (601)	--	SEQ ID NO: 9904				
Consensus (739)						

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FIGURE 3C

								Section 1	
	(1)	1	10	20	30	40	53		
HOBHEGA	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTCCTAGATTATTTCTAGTTAGCTGCAT							
BCV HE	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTCCTAGATTATTTCTAGTTAGCTGCAT							
MHV HE	(1)	-----							
Consensus	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTC TAGATTT TTCTAGTTAGCTGCAT							
								Section 2	
	(54)	54	60	70	80	90	106		
HOBHEGA	(54)	AATTGGTAGCTTAGGTTTTTACAACCTCCTACCAATGTTGTTTCGCATGTAA							
BCV HE	(54)	AATTGGTAGCCTAGGTTTTTGACAATCCTCCTACCAATGTTGTTTCGCATTTAA							
MHV HE	(1)	-----							
Consensus	(54)	AATTGGTAGC TAGGTTTT ACAA CCTCCTACCAATGTTGTTTCGCAT TAA							
								Section 3	
	(107)	107	120	130	140		159		
HOBHEGA	(107)	ATGGACATTGGTTTTTTATTTGCTGACAGTCGTTTCAGATTGTAATCATATTGTT							
BCV HE	(107)	ATGGACATTGGTTTTTTATTTGCTGACAGTCGTTTCAGATTGTAATCATATTGTT							
MHV HE	(1)	-----							
Consensus	(107)	ATGGAGATTGGTTTTTTATTTGCTGACAGTCGTTTCAGATTGTAATCAT TTGTT							
								Section 4	
	(160)	160	170	180	190	200	212		
HOBHEGA	(160)	AATATCAACCCCCATAATTATTCTTATATGGACCTTAATCCTCTTCTGTGTGA							
BCV HE	(160)	ACTACCAACCCCGCTAATTATTCTTATATGGACCTTAATCCTGCTTGTGTGG							
MHV HE	(1)	-----							
Consensus	(160)	A TA CAACCCCC TAATTATTCTTATATGGACCTTAATCCTG TGTGTG							
								Section 5	
	(213)	213	220	230	240	250	265		
HOBHEGA	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTTAGGAGTTTTCACT							
BCV HE	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTTAGGAGTTTTCACT							
MHV HE	(1)	-----							
Consensus	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTTAGGAGTTTTCACT							
								Section 6	
	(266)	266	280	290	300		318		
HOBHEGA	(266)	TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTTTTATGAC							
BCV HE	(266)	TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTTCTATGAG							
MHV HE	(1)	-----							
Consensus	(266)	TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTT TATGAC							
								Section 7	
	(319)	319	330	340	350	360	371		
HOBHEGA	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCAACCGTTCTGGTAGTAA							
BCV HE	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCACCACTTCTGGTAGTAA							
MHV HE	(1)	-----							
Consensus	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCA C TTCTGGTAGTAA							

FIGURE 3C (contd.)

Section 8

	(372)	372	380	390	400	410	424
HOBHEGA	(372)	TGATATTTGGATGCAGAATAAAGGCTTGTTTTTATACTCAGGTTTATAAGAATA					
BCV HE	(372)	TGATATTTGGATGCAGAATAAAGGCTTGTTTTTACACTCAGGTTTATAAGAATA					
MHV HE	(1)	-----ATGGGCAATAAAGCTCGATTTTATGCCCCGAGTGTATGAGAAGA					
Consensus	(372)	TGATATTTGGATGCAGAATAAAGGCTTGTTTTTATACTCAGGTTTATAAGAATA					

Section 9

	(425)	425	430	440	450	460	477
HOBHEGA	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC					
BCV HE	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC					
MHV HE	(44)	TGGCCCAATATAGGAGCCTATCGTTTGTTAATGTGTCTTATGCCTATGGAGGT					
Consensus	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC					

Section 10

	(478)	478	490	500	510	520	530
HOBHEGA	(478)	TCTGCACAATCTACAGCCTTTTGTTAAATCTGGTAGTTTAGTCTTAATAAACC					
BCV HE	(478)	TCTGCACAATCTACAGCCTTTTGTTAAATCTGGTAGTTTAGTCTTAATAAACC					
MHV HE	(97)	AATGCAAAGCCCGCCTCCATTTGCAAGACAATACTTTAACACCTCAATAAACC					
Consensus	(478)	TCTGCACAATCTACAGCCTTTTGTTAAATCTGGTAGTTTAGTCTTAATAAACC					

Section 11

	(531)	531	540	550	560	570	583
HOBHEGA	(531)	TGCATATATAGCTCCTCAAGCTAACTCTGGGGATTATTATTATAAGGTTGAAG					
BCV HE	(531)	TGCATATATAGCTCGTGAAGCTAATTTTGGGGATTATTATTATAAGGTTGAAG					
MHV HE	(150)	CACCTTCATATCGAAGGAGTCTAATTATGTTGATTATTACTATGAGAGTCAGG					
Consensus	(531)	TGCATATATAGCTCTGAAGCTAATTGGGGATTATTATTATAAGGTTGAAG					

Section 12

	(584)	584	590	600	610	620	636
HOBHEGA	(584)	CTGATTTTATTATTGTGAGGTTGTGACGAGTATATCGTACCACTTTGTATTTT					
BCV HE	(584)	CTGATTTTATTATTGTGAGGTTGTGACGAGTATATCGTACCACTTTGTATTTT					
MHV HE	(203)	CTAATTTCACTAGAAAGGTTGTGATGAATTTATAGTACCGCTCTGTGGTTTT					
Consensus	(584)	CTGATTTTATTATTGTGAGGTTGTGACGAGTATATCGTACCACTTTGTATTTT					

Section 13

	(637)	637	650	660	670	689
HOBHEGA	(637)	AACGGCAAGTTTTTG-----TCGAATACA-----AAGTATTATGATGA				
BCV HE	(637)	AACGGCAAGTTTTTG-----TCGAATACA-----AAGTATTATGATGA				
MHV HE	(256)	AATGGCCATTCCAAGGGCAGCTCTTCGGATGCTGCCAATAAATATTATACTGA				
Consensus	(637)	AACGGCAAGTTTTTGTCGAATACA-----AAGTATTATGATGA				

Section 14

	(690)	690	700	710	720	730	742
HOBHEGA	(675)	TAGTCAATATTATTTTAAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA					
BCV HE	(675)	TAGTCAATATTATTTTAAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA					
MHV HE	(309)	CTCTCAGAGTTACTATAATATGGATATGGTGTCTTATATGGGTTCAATTCTA					
Consensus	(690)	TAGTCAATATTATTTTAAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA					

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FIGURE 3C (contd.)

							Section 15
	(743)	743	750	760	770	780	795
HOBHEGA	(728)	C	-----AGAAACCATTACGA-----	-----CTGGTTTTGATCTTAATTGTTAT			
BCV HE	(728)	C	-----TGAAACCATTACCA-----	-----CTGGTTTTGACTTTAAATTGTCAT			
MHV HE	(362)	C	CTTGATGTTGGCAACACTGCTAAGGATCCGGGTCTTGATCTCACTTGCAGG				
Consensus	(743)	C	TGAAACCATTACCA	CTGGTTTTGATCTTAATTGT	AT		
							Section 16
	(796)	796	810	820	830		848
HOBHEGA	(766)	T	ATTTAGTTTTACCCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT				
BCV HE	(766)	T	ATTTAGTTCTACCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT				
MHV HE	(415)	T	ATCTTGCAATTGACTCCTGGTAATTATAAGGCTGTGTCTTAGAATATTTGTT				
Consensus	(796)	T	ATTTAGTTTTACCCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT				
							Section 17
	(849)	849	860	870	880	890	901
HOBHEGA	(819)	A	ACTGTTCTTACGAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCCTG				
BCV HE	(819)	A	ACTGTTCTTACTAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCCTG				
MHV HE	(468)	A	AGCTTACCCTCAAAGGCTATTTGCCCTCCATAAGACAAAGCGCTTTATGCCCTG				
Consensus	(849)	A	ACTGTTCTTAC AAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCCTG				
							Section 18
	(902)	902	910	920	930	940	954
HOBHEGA	(872)	T	ACAGGTTGTTGATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACC				
BCV HE	(872)	T	ACAGGTTGTTGATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACC				
MHV HE	(521)	T	GCAGGTAGTTGACTCAAGGTGGAGTAGCATCCGCCAGTCAGACAATATGACC				
Consensus	(902)	T	ACAGGTTGTTGATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACC				
							Section 19
	(955)	955	960	970	980	990	1007
HOBHEGA	(925)	G	CGGTTGCTTGTCAAAGCTCCGTA CTGTTATTTTCGTAATTCTACTACCAACTA				
BCV HE	(925)	G	CAGTTGCTTGTCAAACCCCGTACTGTTATTTTCGTAATTCTACTACCAATTA				
MHV HE	(574)	G	CTGCAGCCTGTCTAGCTGCCATATTGTTTCTTTTCGCANACATCTGCGAATTA				
Consensus	(955)	G	CTTGCTTGTCAAACC CCGTACTGTTATTTTCGTAATTCTACTACCAATTA				
							Section 20
	(1008)	1008	1020	1030	1040	1050	1060
HOBHEGA	(978)	T	GTTGGTGTTT - - -ATGATATTAATCATGGAGATGCTGGTTTTACTAGCATAAC				
BCV HE	(978)	T	GTTGGTGTTT - - -ATGATATCAATCATGGGATGCTGGTTTTACTAGCATAAC				
MHV HE	(627)	T	AGTGCTGGCACACATGATGCGCACCATGGTGATTTTCATTTCAGGCAGTTAT				
Consensus	(1008)	T	GTTGGTGTTT ATGATAT AATCATGG GATGCTGGTTTTACTAGCATAAC				
							Section 21
	(1061)	1061	1070	1080	1090	1100	1113
HOBHEGA	(1028)	T	TAGTGTTTTGTTATATAATTCACCTTGTTTTTCGCAGCAAGGCGTTTTTAGG				
BCV HE	(1028)	T	CAGTGTTTTGTTATATGACTCACCTTGTTTTTCGCAGCAAGGTGTTTTTAGG				
MHV HE	(680)	T	GCTTGTTTTGTTATATAATGTTTCCTGTATTGCCAGCAGGGTGCAATTTCTT				
Consensus	(1061)	T	AGTGTTTTGTTATATAATTCACCTTGTTTTTCGCAGCAAGGTGTTTTTAGG				

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FIGURE 3C (contd.)

Section 22

	(1114)	1114	1120	1130	1140	1150	1166
HOBHEGA (1081)		TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGTCOCAC					
BCV HE (1081)		TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGCOCTAC					
MHV HE (733)		TATAATAAATGTTAGTTCCTCTTGGCCAGCCTATGGGTACCGTCATTGTCCAAC					
Consensus (1114)		TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCC				TATGGCAGATGTCC	AC

Section 23

	(1167)	1167	1180	1190	1200	1219
HOBHEGA (1134)		TGCTGCTGATATTAATAACCCCTGATTTACCCATTTGTGTGTATGATCCGCTAC				
BCV HE (1134)		TGCTGCTGATATTAATAACCCCTGATGTACCTATTTGTGTGTATGATCCGCTAC				
MHV HE (786)		GGCAGCTAACATTGGTTA - - - TATGGCACCTGTTTGTATCTATGACCCCTCTCC				
Consensus (1167)		TGCTGCTGATATTAATAACCCCTGATGTACCTATTTGTGTGTATGATCCGCTAC				

Section 24

	(1220)	1220	1230	1240	1250	1260	1272
HOBHEGA (1187)		CAGTTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT					
BCV HE (1187)		CAATTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT					
MHV HE (836)		CGGTCATACTGCTAGCTGTGTTATTGGGTATAGCTGTGTGATTATTGTGTTT					
Consensus (1220)		CAGTTATTTTGCTTGGCATTCTTTTGGGTGTTGCGGTCATAATTATTGTAGTT					

Section 25

	(1273)	1273	1280	1290	1300	1310	1325
HOBHEGA (1240)		TTGTTGTTATATTTTATGGTGGATAATGGTACTAGGCTGCATGATGCTTAGAC					
BCV HE (1240)		TTGTTGTTATATTTTATGGTGGATAATGGTACTAGGCTGCATGATGCTTAGAC					
MHV HE (889)		TTGATGTTTTATTTTATGACGGATAGCGGTGTTAGATTGCATGAGGCATAA - -					
Consensus (1273)		TTGTTGTTATATTTTATGGTGGATAATGGTACTAGGCTGCATGATGCTTAGAC					

Section 26

	(1326)	1326	1337	
HOBHEGA (1293)		CATAATCTAAAC		SEQ ID NO: 9913
BCV HE (1293)		CATAATCTAAAG		SEQ ID NO: 9885
MHV HE (940)		- - - - -		SEQ ID NO: 9896
Consensus (1326)		CATAATCTAAAC		

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FIGURE 4**FIGURE 4A**

		Section 1			
		(1) 1	10	20	39
avian infectious bronchitis pol 1ab	(1)	-----			
bovine coronavirus pol 1ab	(1)	MSKINKYGLLELHWAPEFPWMFEDAEEKLDNPSSEVDIV			
Human corona 229E pol 1ab	(1)	-----MACNRVTLAVASDSEISANG			
Murine hepatitis pol 1ab	(1)	MAKMGKYGLGFRKWAPEFPWMLPNASEKLGNEPERSHEDGF			
Consensus	(1)	MAKI KYGL WAPFEPWM NA EKL NPDSSD			
		Section 2			
		(40) 40	50	60	78
avian infectious bronchitis pol 1ab	(1)	-----			
bovine coronavirus pol 1ab	(40)	CSTTAQKLEETGGICPENHVMMDCRRLLKOECCVQSSLEIR			
Human corona 229E pol 1ab	(21)	CSTIAQAVRRYSEAAASNGFRACRFVSLDLDQCI VGIADD			
Murine hepatitis pol 1ab	(40)	GPSAAQEPKVKCKTLVNHVRVNC SRLPALECCVQSATIR			
Consensus	(40)	CST AQ LK G NHVRV C RLL LECCVQSAILR			
		Section 3			
		(79) 79	90	100	117
avian infectious bronchitis pol 1ab	(1)	-----			
bovine coronavirus pol 1ab	(79)	ETVMNTRPYDLEVLLODAIOSREAVLVTEPLGMSIEACY			
Human corona 229E pol 1ab	(60)	TYVMGLHGNOTLFCNIMKFSDRPFMLHG-----WLVTFS			
Murine hepatitis pol 1ab	(79)	DIFVDEDEPKVLEASTMMALQFGSAVLVKPSKRLSIOAWT			
Consensus	(79)	DIVM PN LE IMAIQ R AVL V P LSI AFS			
		Section 4			
		(118) 118	130	140	156
avian infectious bronchitis pol 1ab	(1)	----MASSLKQGVSPK-----PRDVILVSKDI			
bovine coronavirus pol 1ab	(118)	VRGCNENGWMTMGLFRRRSVGNTGRCAVNKHVAYOLYIMID			
Human corona 229E pol 1ab	(93)	NSNYLLEEDVVFGR-----GGGNVTYTDQYL CGADG			
Murine hepatitis pol 1ab	(118)	NLGVLPKTAAMGLFKRVCLGNTRECS CDAHVVAEHLFTVQ			
Consensus	(118)	N G LP SF MGLFKR LCNTG CAV HVAYLLF D			
		Section 5			
		(157) 157	170	180	195
avian infectious bronchitis pol 1ab	(24)	PEQLCDALFFYTSHNPKDYADAEAVRQKFDRSLQTGKQF			
bovine coronavirus pol 1ab	(157)	PAGVCFGAGQFVGWVPLPLAFMPVOSRKFIVPWVMYLRKC			
Human corona 229E pol 1ab	(126)	KPVMSDDLWQFVDHEGENEETIINGHTYVCAWLTKRKPL			
Murine hepatitis pol 1ab	(157)	PDGVCLGNGRFICWFEVPTAIREYAKQWLQPMSTLLRKG			
Consensus	(157)	PDGVCDGLGQFVGWFIPL AIPINARQFI PWLI LKK			
		Section 6			
		(196) 196	210	220	234
avian infectious bronchitis pol 1ab	(63)	KFET-----VC--GLFLLKGVDPKITPGVPAKV			
bovine coronavirus pol 1ab	(196)	GEKG-AYNKDHKRGGFHVNFKVEDAYDLVHDEPKGKE			
Human corona 229E pol 1ab	(165)	DKR-----Q--NNLAIEETIYMHGDALHTLR			
Murine hepatitis pol 1ab	(196)	GNKGSVTSGHFRRAVTMPVYDFNVEDACEEVHLNPKGKY			
Consensus	(196)	GFKG KRA M VYNL VEDA DLVHDAPKGKE			

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FIGURE 4A (contd.)

Section 7						
	(235)	235	240	250	260	273
avian infectious bronchitis pol 1ab	(88)	LKATSKLADLEDIFGVSPILARKYRELLKTACOWSLTVEA				
bovine coronavirus pol 1ab	(234)	SKKAYALIRGYRGVKPILLYVDQYGCDDYTGGLADGLEAYA				
Human corona 229E pol 1ab	(190)	NGSVLEMAKEVKTSKVVLSDALDKLYKVFGSPVMTNGS				
Murine hepatitis pol 1ab	(235)	SCKAYALLKGYRGVKPILFVDOYGCDDYTGCLAKGLEDDYG				
Consensus	(235)	SKKAYALAKGYRGVKPILLVDQYGCCLYTGA LA GLT YA				
Section 8						
	(274)	274	280	290	300	312
avian infectious bronchitis pol 1ab	(127)	LDVRAQTLDEIFDPTEILWLQVAAKIHVSSMAMRRRLVGE				
bovine coronavirus pol 1ab	(273)	DKTLQEMKALFPIWSDLPFDVTVAWHVVRDPRYVMRLQ				
Human corona 229E pol 1ab	(229)	NILEAFTKPVFISALVQCTCGTKSWSVGDWTGFKSSCCN				
Murine hepatitis pol 1ab	(274)	DITLSEMKELFVWRDSDLSEVLVAWHVDRDPRRAAMRLQ				
Consensus	(274)	DITLAETKDLFPIWSD L DV VAWHVDRDPRKAMRLQ				
Section 9						
	(313)	313	320	330	340	351
avian infectious bronchitis pol 1ab	(166)	VTAKVMDALGSNLSALFQIVKQQTARI FORALAI FENVN				
bovine coronavirus pol 1ab	(312)	SASTIRSMAYVANPTEDLCDGSSVVIKEPVHNYADDSFLL				
Human corona 229E pol 1ab	(268)	VISNKLQVVPGNVKGDAVITTOQAGAGTRYFCGMTLKF				
Murine hepatitis pol 1ab	(313)	TLATVRCIDYVCGPTEDVVDGCVVVRFAHLLAANAIVK				
Consensus	(313)	VIATVRCVLYVNQPTEDLVDGSVVAREPIKLLAA SIV				
Section 10						
	(352)	352	360	370	380	390
avian infectious bronchitis pol 1ab	(205)	ELEFORIAALKMAFAKCARSLTVVVVERTLVVKEFAGTCL				
bovine coronavirus pol 1ab	(351)	RQHNLYDIMSCFYMEADAVVNAFYGVDLKDCGFVMOEGY				
Human corona 229E pol 1ab	(307)	VAN-----IEGVSVWRVTALQSVDCFVASSTEVE				
Murine hepatitis pol 1ab	(352)	RLP---RLVETMLYTDSSVTEFCYKTKLCECGFITQEGY				
Consensus	(352)	RLPN I IL FIEAASVI VIYL KL DCGFISQFGY				
Section 11						
	(391)	391	400	410	429	
avian infectious bronchitis pol 1ab	(244)	ASINGAVAKTFEELPNGFMGSKIFTTLAFFKEAAVRVVE				
bovine coronavirus pol 1ab	(390)	IDCEQDLQDKGWVPGNMIDGEACTTCGHVYETGDLLEAQ				
Human corona 229E pol 1ab	(336)	EEHVNRMDTLCFNVRNSVTDECRLAMTCAEMTSNVRROV				
Murine hepatitis pol 1ab	(388)	VDCCGDTCDRGWVAGNMMDGFPCFGCTKNYMPWELEAQ				
Consensus	(391)	IDC GDLCDFKGWVPNNMMDGF CTTLG YESAVRLAQ				
Section 12						
	(430)	430	440	450	468	
avian infectious bronchitis pol 1ab	(283)	NIPNAPRGTKGFEEVVGNAKGTQVVVRGMRNDLTLLDOKA				
bovine coronavirus pol 1ab	(429)	SSGVLPVNFVLTHTKSAAGYGGFGCKDSETLYGQTVVYFG				
Human corona 229E pol 1ab	(375)	ASGVLDISTGWFDDYDDIFAE-----SK-PWFVRKA				
Murine hepatitis pol 1ab	(427)	SSGVIREGGVLETTQSTDVTN----RESEKLYGHAVVPFG				
Consensus	(430)	SSGVIPIGTVLFTVSADAFG KDSFKLYG VV KA				

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FIGURE 4A (contd.)

Section 13						
	(469)	469	480	490	507	
avian infectious bronchitis pol 1ab	(322)	DIPVEPEGWSAII LDGHL CYVFRSGDRFYAAPLSGNEFALS				
bovine coronavirus pol 1ab	(468)	GCVYWS-PARNIWIPI LKSSVKSYDGLVYTGTVGCKATV				
Human corona 229E pol 1ab	(405)	EDIFGP-CWSALASALKQLKVTTGELVRFVKSTICNSAVA				
Murine hepatitis pol 1ab	(462)	SAVYWS-PCPGMWLPVITWSSVKSYSGLT YTGTVGCKATV				
Consensus	(469)	D VYWS PWSAIWIPI L SSVKSYDGL YTGTVGNKAIV				
Section 14						
	(508)	508	520	530	546	
avian infectious bronchitis pol 1ab	(361)	DVHCCERVVCLSDGMTPEINDGLILAAIYSSFSVSELVT				
bovine coronavirus pol 1ab	(506)	KETNLICKALYLDYVQHKCGNLHORELLGVSEVWHKQLL				
Human corona 229E pol 1ab	(443)	VMGGTICQILASVPEKFLNAFDVFTATQTVFCVETCT				
Murine hepatitis pol 1ab	(500)	QETDAICRSLYMDYVQHKCGNLEQRAILLGLDDVYHQLL				
Consensus	(508)	VT ICRSLYLDYVQHKCGNL QRAILGVSDVWHEQLT				
Section 15						
	(547)	547	560	570	585	
avian infectious bronchitis pol 1ab	(400)	ALKKCEPFKFLGHKFVYAKDAAVSFTLAKAATIAADVLR				
bovine coronavirus pol 1ab	(545)	INRGVYKPLEENTDYENMRRAKFSLETETVCADGIMBFL				
Human corona 229E pol 1ab	(482)	TAGKAFDKVFDYVLLDNALVKLVTTKIKGVRRERGINVKR				
Murine hepatitis pol 1ab	(539)	VNRGDYSLIDENVDLFVKRRAEFACK-FATCGDGLVPLL				
Consensus	(547)	INRKAY LLENVDLFNARRA VS KLEAVCADGLVPLL				
Section 16						
	(586)	586	600	610	624	
avian infectious bronchitis pol 1ab	(439)	FOSARVIAEDVWSEFTEKSFEFWKELAYGKVRNLEEFVKT				
bovine coronavirus pol 1ab	(584)	LDDLVPRAVYLAVEGQAFCDYADKICHAVVSKSKELLDV				
Human corona 229E pol 1ab	(521)	YATVVVGSTEEVKS-----RVERSTAVLTIANYSKL				
Murine hepatitis pol 1ab	(577)	LDGLVPRSYYLIKSGQAFSTMMVNFSEHVTDMCMDALL				
Consensus	(586)	LDSLVRAYYLIKSGQAFS VKISHAVVSIA EMSKL				
Section 17						
	(625)	625	630	640	650	663
avian infectious bronchitis pol 1ab	(478)	YVCKAQMSIVILA AVLGEDIWHDVS---QVLYKLGVLFT				
bovine coronavirus pol 1ab	(623)	SLDSLAAIHYLNSKI VDLAQHFSDFGTSFVSKIVHFFK				
Human corona 229E pol 1ab	(554)	FDEGYTVVVGDMAYFVSDGYERLMASPNVLTAVYKPL				
Murine hepatitis pol 1ab	(616)	FMHDVKKVATKYVKKVTGKLAVRFKALGVAVVRKLTENED				
Consensus	(625)	FLD LSAI YLAAVIGDLAFLMA G SVVSKIVHFF				
Section 18						
	(664)	664	670	680	690	702
avian infectious bronchitis pol 1ab	(514)	KVVD FCDKHWKGF CVOLKRAKLIVTETFCVLKGV AQHCF				
bovine coronavirus pol 1ab	(662)	TFTTSTAIAFAWVLEHVLHGAYIVVESDIYFVKNI PRYA				
Human corona 229E pol 1ab	(593)	FAFNVNVMGTRPEKEPTTVTCENLES AVL EVNDKITEEQ				
Murine hepatitis pol 1ab	(655)	LAVDIAASAAGWLCYQLVNGLEAVANGVITFVQEMPELV				
Consensus	(664)	AVDI ALAFKWLCFQLL G FIV EAVIFFV IPEF				

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FIGURE 4A (contd.)

						Section 19
	(703)	703	710	720	730	741
avian infectious bronchitis pol 1ab	(553)	QLLLDAIHSLYKSFKKCALGRTHGDLLEFWKGGVHKIVQD				
bovine coronavirus pol 1ab	(701)	SAVAQAFRSVAKVVLDLSLRTFIDGLSCFKIGRRRTICLS				
Human corona 229E pol 1ab	(632)	LDYSIDVIDNEILVKPNISLCVPLYVRDYVDKWDDFCRQ				
Murine hepatitis pol 1ab	(694)	KNEVDKFKATFFKVLIDSMVSSTLSGLTVVKTA SNRVCLIA				
Consensus	(703)	VSDAFKSLFKVVKDSISVSII GLS FK G RICLA				
						Section 20
	(742)	742	750	760	770	780
avian infectious bronchitis pol 1ab	(592)	GD-----				
bovine coronavirus pol 1ab	(740)	GSKIYEVERGLLHSSQLRLDVYDLIMPSSQVQKAKQKPIY				
Human corona 229E pol 1ab	(671)	YS-----				
Murine hepatitis pol 1ab	(733)	GSKVYEVVQKSTISA YVMPVGCSEATCLVGEIEP-----				
Consensus	(742)	GSKIYEV	L A LPL	D T		
						Section 21
	(781)	781	790	800		819
avian infectious bronchitis pol 1ab	(594)	-----EIIWFDATDSVDVEDIGVVQEKSIDFEVCD				
bovine coronavirus pol 1ab	(779)	LKSGSGDFSLADSVVEVVTTSLTPCGYSEFPKVVADKIGI				
Human corona 229E pol 1ab	(673)	-----NESWFEDDYRAFTSVLDITDAAVKAAESKA				
Murine hepatitis pol 1ab	(766)	-----AVFEDDVVDVVKAPLLYQGCKPPTSFEKIGI				
Consensus	(781)		EDWVVDVVS A LT LGISDPPSTADKICI			
						Section 22
	(820)	820	830	840		858
avian infectious bronchitis pol 1ab	(623)	DVTLPENQPGH MVQIEDDGKNYMEFFREKKDENIYYTPMS				
bovine coronavirus pol 1ab	(818)	VDNVYMAKAGDKYYPVVVDG-HVGLLDQAWRVPCAGRRV				
Human corona 229E pol 1ab	(703)	FVDTIVPPQPSILKVIDGGKIWNGVTKNVNSVRDWLKS L				
Murine hepatitis pol 1ab	(798)	VDKLYMAKCGDQFYPVVVDNDTVGVLDQCWRFFPCAGKRV				
Consensus	(820)	VV LYMAKCGDIVYPVVVGK WVGVL DQ WRVPCAGKKV				
						Section 23
	(859)	859	870	880		897
avian infectious bronchitis pol 1ab	(662)	QLGAINVVCKAGGKTVTFGETTVQELPPPDVVPIKVSIE				
bovine coronavirus pol 1ab	(856)	TFKEQPTVNETASTPKTIKVFYELDKDENTILNTACGVF				
Human corona 229E pol 1ab	(742)	KLNLTOQGILLGTCAKRFRKRWLGILLLEAYNAFLDTVVSTV				
Murine hepatitis pol 1ab	(837)	EFNDKPKVRKIPST-RKIKITFALDATFDSVLSKACSEE				
Consensus	(859)	LND P V KIAST RTIKITFILD ENSVL TAVSIF				
						Section 24
	(898)	898	910	920		936
avian infectious bronchitis pol 1ab	(701)	CCGEPWN-----TTFKKAYKEPIEVDTLTVEQLLSV				
bovine coronavirus pol 1ab	(895)	EVDDTVDMEEFYAVVIDAIEEKLSPCKELEGVCAKVS AF				
Human corona 229E pol 1ab	(781)	KIGG-----LTFKTYAFDKPYIVIRDIVCKV				
Murine hepatitis pol 1ab	(875)	EVDKDYTLDEL LDVLDVLDVESTLS PCKEHDVIGTKVCAL				
Consensus	(898)	EVGD V LDE VVIDAIE TLSPCKEHDVIGDKVCAV				

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FIGURE 4A (contd.)

Section 25						
	(937)	937	950	960	975	
avian infectious bronchitis pol 1ab	(733)	IYEKMCDDLK	FPEAPEPPPFEN	VALVDKNGRI	LDQIKS	
bovine coronavirus pol 1ab	(934)	LQKLEDNSLE	DEAGREVLASKLY	CAFTAPEDDDFLEE		
Human corona 229E pol 1ab	(807)	ENKTEAEWLE	PPHNDRIKSFST	FESAYMPIADP	THFDI	
Murine hepatitis pol 1ab	(914)	LDRLAGDYVYL	DEGGDEVIAPRM	YCFSFAPD	EDCVAA	
Consensus	(937)	LNKLEADWLF	LFPEAGEEVIF	SKLYCAFSAP	DDDDCIDA	
Section 26						
	(976)	976	990	1000	1014	
avian infectious bronchitis pol 1ab	(772)	CHLIYRDYES	DDDI E E E D A E E C D T D S G E A E E C D T N	----	----	
bovine coronavirus pol 1ab	(973)	SGVEEDDVE	GEETDLTVTSAGE	PCVASEQEE	----	
Human corona 229E pol 1ab	(846)	EEVELLDAA	FVEPGCGGITAV	IDEHVFYKKDG	VYYP----	
Murine hepatitis pol 1ab	(953)	DVVDADENQ	DDDAEDSAVLV	ADTQEE	DGVAKQVEADSE	
Consensus	(976)	DVE	DD E DD	DDSAILAADD	DA E EEG	
Section 27						
	(1015)	1015	1020	1030	1040	1053
avian infectious bronchitis pol 1ab	(807)	-----	SECEE	DEDTKVLALI	QDPASIKYPL	PLEDE
bovine coronavirus pol 1ab	(1004)	-----	SSEILED	TLDGPCVET	SDSOVEED	VEMSDFADLE
Human corona 229E pol 1ab	(882)	-----	SNGTNILP	VAFKAAGGKV	SFSDQVEV	KDIEPVY
Murine hepatitis pol 1ab	(992)	ICVAHTGS	QELAEFPDAV	GSQTPIASAE	ETEVEGEAS	DRE
Consensus	(1015)	S	SEDL	EDD	AA A IQ	AEDVEV D ADLE
Section 28						
	(1054)	1054	1060	1070	1080	1092
avian infectious bronchitis pol 1ab	(838)	YSVYNGCIV	HKDAIDMVNLP	SG	-----	-----
bovine coronavirus pol 1ab	(1039)	SVIQDYENVC	FEFYTTEP	-----	-----	-----
Human corona 229E pol 1ab	(916)	RVKLCFEFE	DEKLVDVCEKA	IG	-----	-----
Murine hepatitis pol 1ab	(1031)	GIAEAKATV	CADAVDACPDQ	VEAFEIEKVED	SILDELQT	
Consensus	(1054)	VI	FE VC	DAVDVCP	IG	
Section 29						
	(1093)	1093	1100	1110	1120	1131
avian infectious bronchitis pol 1ab	(860)	-----	-----	-----	-----	EE
bovine coronavirus pol 1ab	(1057)	-----	-----	-----	-----	EFVKV
Human corona 229E pol 1ab	(938)	-----	-----	-----	-----	KKIK
Murine hepatitis pol 1ab	(1070)	ELNAPADKTY	EDVLAFDAVC	SEALS	SAFYAVPS	DETHFKV
Consensus	(1093)					KV
Section 30						
	(1132)	1132	1140	1150	1160	1170
avian infectious bronchitis pol 1ab	(862)	TFVVN	-----	-----	NCFEGAVKPL	PQKVVDV
bovine coronavirus pol 1ab	(1062)	LDLYVPKATR	NNCWLRSVLAV	MQKLE	CQFKDKNLQD	LWV
Human corona 229E pol 1ab	(942)	HEG	-----	DWDSFCKTI	QSALSVVSCY	VNLPTYI
Murine hepatitis pol 1ab	(1109)	CGFYSPAIE	R TNCWLRS	T L I V M O S L P L E F K D L E M Q K L W L		
Consensus	(1132)	DLY P	R NCWLRS	L VMQALPL	FKDLNLQ	LWV

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FIGURE 4A (contd.)

Section 31					
	(1171)	1171	1180	1190	1209
avian infectious bronchitis pol 1ab (884)		LGDWGEAVDAQEQLCQQEELQHTFEEFVENSTGSSKMT			
bovine coronavirus pol 1ab (1101)		LYKQQYSOLFVDTLVNKTLANTVVPQGGYVADFAFWELT			
Human corona 229E pol 1ab (972)		YDEEGGNDLSLPVMISEWLSVQQAQQEATLPDIAEDVV			
Murine hepatitis pol 1ab (1148)		SYKAGYDQCFVDKLVKSVKSTIILPQGGYVADFAFFELS			
Consensus (1171)		LYK GYAQLFVD LVN IPLSIILPQGGYVADFAFFFLT			
Section 32					
	(1210)	1210	1220	1230	1248
avian infectious bronchitis pol 1ab (923)		EQVVVEDQELPVVEQLQDVVVYTPDLEVAKETAEEVDE			
bovine coronavirus pol 1ab (1140)		LCDWQCVAYWKCICLALKKLKGLDAMFFYGDVVSHVCK			
Human corona 229E pol 1ab (1011)		DQVEEVNSIEDIETVVKHDVSPFEMPEEELNGLKILKQ			
Murine hepatitis pol 1ab (1187)		QCSFKAYANWRCLFCMELKLOGLDAMFFYGDVVSHMCK			
Consensus (1210)		DQVF A WKCIECDLCLKL GLDAMFFYGDVVSHVCK			
Section 33					
	(1249)	1249	1260	1270	1287
avian infectious bronchitis pol 1ab (962)		FILIFAVPKEEVVSQKDGAIKOEPTQVVKPQRE-KK--			
bovine coronavirus pol 1ab (1179)		CGESMVLIDVDVPETAHFALKKLLFCAFITKRSVYKAAC			
Human corona 229E pol 1ab (1050)		LDNNCWVNSVMLQIQLTGILDGDYAMQFFKMG-----			
Murine hepatitis pol 1ab (1226)		CGNSMTLLSADIFVTEHFQVRDDKFCAFYTPRKVFRAAC			
Consensus (1249)		CGNSM LISVDVPFTLHGALKDD FCQFVTPRKVFKAAC			
Section 34					
	(1288)	1288	1300	1310	1326
avian infectious bronchitis pol 1ab (998)		-----AK			
bovine coronavirus pol 1ab (1218)		VVDVNDSHSMAVVDGKQIDDHRTSITSDFEDFIIGHGM			
Human corona 229E pol 1ab (1082)		-----			
Murine hepatitis pol 1ab (1265)		AVDVNDCHSMAVVEGKQIDGKVVTKFIGDKFEDMVGYGM			
Consensus (1288)		VDVND HSMVVDGKQID VT DKFDFIIGHGM			
Section 35					
	(1327)	1327	1340	1350	1365
avian infectious bronchitis pol 1ab (1000)		KFKVKPATCEKPKFLEYKTCVGDLTVVLAKAIDDEFKEFC			
bovine coronavirus pol 1ab (1257)		SFSMTTFEIAQLYGSCITPNVCFVKGDIIKVSQRVKAEV			
Human corona 229E pol 1ab (1082)		-----RVAKMIERCYTAEQCIRGAMGDVGLCMYRLIK			
Murine hepatitis pol 1ab (1304)		TFSMSPFELAQLYGSCITPNVCFVKGDVIKVVRLVNAEV			
Consensus (1327)		SFSMSPFEIAQLYGSCYTPNVCFVKGDIIKVLKLVKAEV			
Section 36					
	(1366)	1366	1380	1390	1404
avian infectious bronchitis pol 1ab (1039)		LVNAANEHMTHGSGVAKAIAIDFCGLDFVEYCEDYVKKH			
bovine coronavirus pol 1ab (1296)		VVNPAANGHMAHGGGVAKAIAVAAGQOFVKETTTDMVKSQ			
Human corona 229E pol 1ab (1114)		DLHTGFMVNDYKCSCTSGRLEESCAVLECTPTKKAPPYQ			
Murine hepatitis pol 1ab (1343)		IVNPAANGHMAHAGAGVAGATAEKACSAFIKETSDMVKAQ			
Consensus (1366)		IVNPAANGHMAHAGAGVAKAIAE AGA FVKETTTDMVKAH			

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FIGURE 4A (contd.)

						Section 37
	(1405)	1405	1410	1420	1430	1443
avian infectious bronchitis pol 1ab (1078)	PQOR	-----	-----	-----	-----	-----
bovine coronavirus pol 1ab (1335)	VCATGDCYVSTGGKLC	KTVLNVVGP	DARTQGK	OSYALLE		
Human corona 229E pol 1ab (1153)	TCLNCNAPRMCTIRQL	QGTII	EVQQKPEP	-----	VNP	
Murine hepatitis pol 1ab (1382)	VCQVGECEYESAGGKLC	KKVLNIVGP	DARGHGK	OCYSTLE		
Consensus (1405)	VCQ	GDCY S	GGKLC	VLNIVGP	DAR	GKQ YALLE
						Section 38
	(1444)	1444	1450	1460	1470	1482
avian infectious bronchitis pol 1ab (1082)	-----	-----	-----	-----	-----	-----
bovine coronavirus pol 1ab (1374)	RVYKHLNKYDCVVTTL	ISAGIFSV	PSDVSL	TYLLGTA	EK	
Human corona 229E pol 1ab (1185)	VSEFVVKPVQSSIFRG	AVSCHYQ	TNIYSQ	NLCVDG	FGVNV	
Murine hepatitis pol 1ab (1421)	RAYOHINKCDNVVTTL	ISAGIFSV	PTDVSL	TYLLGV	VTK	
Consensus (1444)	RAY	HINKCD	VVTTL	ISAGIFSV	PSDVSL	TYLLG L K
						Section 39
	(1483)	1483	1490	1500	1510	1521
avian infectious bronchitis pol 1ab (1110)	KIVAAYKNVLVDG	VVNYVVP	VL	SLGIFG	VDFKMSI	DAMR
bovine coronavirus pol 1ab (1413)	QMVLVSNNOEDFDL	ISKCOIT	AVEG	TKKLA	ERLSFN	VGR
Human corona 229E pol 1ab (1224)	KIQPWTN-----	DALNTT	CIKD	ADYN	AKMET	SVTPIK
Murine hepatitis pol 1ab (1460)	NVFLVSNNOEDFDV	IEKCOV	TSVACT	KALS	LOLAK	NLCR
Consensus (1483)	KVV	LVSNNO	DDFDV	IAKCQIT	LV	DGTRKALALKLSINLIR
						Section 40
	(1522)	1522	1530	1540	1550	1560
avian infectious bronchitis pol 1ab (1149)	BAFEGCTIRVL	LES	-----	-----	-----	-----
bovine coronavirus pol 1ab (1452)	STVYETDANKLL	LSNDVA	EVSTF	NVLQD	VL	SLRHDIALD
Human corona 229E pol 1ab (1256)	NTVDTTTPKEEF	VVKEK	LN	AF	LVHDN	VAFYQGDVD
Murine hepatitis pol 1ab (1499)	DNKEVTINACSS	LES	-----	ESCE	VSSSYD	VLQEV
Consensus (1522)	DIVF	T A	LLFS	DL	EVSSHD	VLQDV ALRHD
						Section 41
	(1561)	1561	1570	1580		1599
avian infectious bronchitis pol 1ab (1163)	-----	-----	-----	-----	-----	-----
bovine coronavirus pol 1ab (1491)	DDARTFVQSNVDV	VPEGWR	VVNKF	YQING	VRTV	KYFECP
Human corona 229E pol 1ab (1295)	VDFFDFIVNA	ANENLA	HGGGL	AKALD	VYTKG	KLQRLSKEH
Murine hepatitis pol 1ab (1537)	DDARFVQANMD	CLPTD	WRLV	NKEDS	V	DGVRTIKYFECP
Consensus (1561)	DDAR	FVQANMD	LP	GWRLV	NKFD	I GVRTIKYFECP
						Section 42
	(1600)	1600	1610	1620		1638
avian infectious bronchitis pol 1ab (1163)	--LSQEHID	-----	-----	YFD--	VTCKOK	TLY
bovine coronavirus pol 1ab (1530)	GGIDTICSQDK	VFGYV	QQGS	FNKAT	VAQIK	ALFEDKVDIL
Human corona 229E pol 1ab (1334)	IGLAG-----	-----	KVKV	GTG	VMVE	CDLSLRI
Murine hepatitis pol 1ab (1576)	GGTFVSSQ	GKKEGY	VQNGS	FEASV	SQIR	ALLANKVDVH
Consensus (1600)	GGIAI	SQDK	FGYVQ	NGSEK	ATVAQ	IKALS

FIGURE 4A (contd.)**Section 43**

	(1639)	1639	1650	1660	1677
avian infectious bronchitis pol 1ab (1182)	LT	EDGVK	YRSIVL	KPGDSL	CGQFG-----QVYAKN
bovine coronavirus pol 1ab (1569)	LT	VDGVN	ETNR	FMPV	GESFGKSLGNVECDGVNVTKHKCD
Human corona 229E pol 1ab (1360)	GER	KKEK	HERD	LLIKAY	NTINNEQGTPLTPILSCGIFGIK
Murine hepatitis pol 1ab (1615)	CT	VDGVN	FERS	CCVAE	GEVFGKTLG
Consensus (1639)	LT	VDGVN	FERSIL	VK GES	FGKSLG

Section 44

	(1678)	1678	1690	1700	1716
avian infectious bronchitis pol 1ab (1211)	K	IVFTAD	DDVEDK	ETLYV	PPTDKSILEYYGLDAQKYVIYT
bovine coronavirus pol 1ab (1608)	I	NYKGR	VVEFO	FDNLIS	SEDIKAVRSSFNEDQKELLAYNNM
Human corona 229E pol 1ab (1399)	L	ETSLE	VLLD	VCNTR	KKEVKMFVYTDTEVCKVKDFVSGLVN
Murine hepatitis pol 1ab (1654)	A	IYKGR	VVEFQ	MSLS	SEADLVAVKDAFGEFDEPQLIKYYTM
Consensus (1678)	I	IYKGR	VVEFQF	NLSE	VDL AVSDSF

Section 45

	(1717)	1717	1730	1740	1755
avian infectious bronchitis pol 1ab (1250)	O	T	LAQK	WNVO	YRDNEL
bovine coronavirus pol 1ab (1647)	L	VNCS	KWQV	VFN	CKYFT
Human corona 229E pol 1ab (1438)	V	QKVE	QPKTE	PK-P	VSVIK
Murine hepatitis pol 1ab (1693)	L	G-M	CKWS	V	MVCG
Consensus (1717)	L	M	KWN	V	VFKG

Section 46

	(1756)	1756	1770	1780	1794
avian infectious bronchitis pol 1ab (1289)	R	EKGEL	TEAWAK	LLG-G	DEPTDE
bovine coronavirus pol 1ab (1686)	K	KIVQ	WQEA	WLEERS	GRPAR
Human corona 229E pol 1ab (1476)	C	VADD	KPIV	LETT	DSMLT
Murine hepatitis pol 1ab (1731)	K	EPKW	QWQEA	WNEERS	GKPLR
Consensus (1756)	K	E	K	FQWQEA	W EFRSGK

Section 47

	(1795)	1795	1800	1810	1820	1833
avian infectious bronchitis pol 1ab (1327)	A	NWLD	ANLAE	HFDAD	YTNAF	LEKKRV
bovine coronavirus pol 1ab (1725)	S	RDE	FLRV	VFSQ	VDLT	GALCD
Human corona 229E pol 1ab (1515)	C	VDIN	KATP	-SGN	LKFD	IGSV
Murine hepatitis pol 1ab (1770)	S	IDEM	BRV	L	READ	LSGAT
Consensus (1795)	S	ID	FLRV	V	ADLS	GA C

Section 48

	(1834)	1834	1840	1850	1860	1872
avian infectious bronchitis pol 1ab (1360)	--	YELRG	----	LEAC	IO	PVRAT
bovine coronavirus pol 1ab (1764)	V	MHFG	TLSR	EDLE	IGY	TVDC
Human corona 229E pol 1ab (1551)	D	NNVQ	RCTR	KLNR	LMCD	IVCT
Murine hepatitis pol 1ab (1809)	V	MHFG	TLDK	GDI	V	RGYNI
Consensus (1834)	V	MHFG	TLSR	DLE	IGYNI	VCTC

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FIGURE 4A (contd.)

Section 49						
	(1873)	1873	1880	1890	1900	1911
avian infectious bronchitis pol 1ab (1393)		NNTDEVIEAS	LPYLLLFATDGPATVDCDEDAVGTVVFVG			
bovine coronavirus pol 1ab (1803)		SNTPEASVRLEKGVGSANIFKGDVGHYVHVKCEQSYOLY				
Human corona 229E pol 1ab (1590)		SFVGGLKAAEAKVITIKVTEDEGVNVHDVTVTDDKSEFQQ				
Murine hepatitis pol 1ab (1848)		SNTPEGRKLPDDVVAANFTGGSVGHYTHVKCKPKYOLY				
Consensus (1873)		SNTPELRKLP	VISANITDGGAVVHYVHVKCD			SYOLY
Section 50						
	(1912)	1912	1920	1930	1940	1950
avian infectious bronchitis pol 1ab (1432)		STNSGHCYTOAA	QAFDNIAKORKEFGKKS	PYITAMYTRE		
bovine coronavirus pol 1ab (1842)		DASNVKRVTDVT	NLSDCLYEKNLKOTERSVLITTYLDD			
Human corona 229E pol 1ab (1629)		VGVIADKDKDLS	AMPSDINTSELLTKAIDMDWVEFYGF			
Murine hepatitis pol 1ab (1887)		DACNVNVKVSFAK	NFTDCLYLKNLKOTESSVLITTFYDD			
Consensus (1912)		DA NV	KVTDASGNLSDCLYLKNLKQTFSSVLITTFYLD			
Section 51						
	(1951)	1951	1960	1970		1989
avian infectious bronchitis pol 1ab (1471)		AFKNETSLPVAKQSKGKSKSVKEDVSNLATSSKASFDNL				
bovine coronavirus pol 1ab (1881)		VKKTEYNPDLSQYYCDGCKYYTORLTKAQEKTFEKVDGV				
Human corona 229E pol 1ab (1668)		KDAMTFATVDHSAFAYESAVVNGIRVLKTS DNNCWVNAV				
Murine hepatitis pol 1ab (1926)		VKCVLEKPDLSQYYCESGKYYIKPILKAQFRTEFEKVDGV				
Consensus (1951)		VKKVEYAPDLSQYYCD	SKYYT	IKAQFKTFEKVDGV		
Section 52						
	(1990)	1990	2000	2010		2028
avian infectious bronchitis pol 1ab (1510)		TDFEQWYDSNIYE	SHKVQESP DNFDKYVSETTKEDSKLP			
bovine coronavirus pol 1ab (1920)		YTNFKLIGHITICDILNAKLGFDSSKEF	FYKVTETWPTAT			
Human corona 229E pol 1ab (1707)		CIALQYSKPHFISQGLDAAWNKFVLGD	EIFMAFVYYVA			
Murine hepatitis pol 1ab (1965)		YTNFKLVGHSLAEKLNALGFD	CNSPFTFYKITEWPTAT			
Consensus (1990)		YTNFQLIGHSI	E LNAKLGFD	FVEYKVTETWPTAT		
Section 53						
	(2029)	2029	2040	2050		2067
avian infectious bronchitis pol 1ab (1549)		LTLKVRGKIKSVVDFRSKDGFIYKLTPDTEWSKAPVYYF				
bovine coronavirus pol 1ab (1959)		GDVVLATDDLYVKRYERGCITTEGKPVVWLSHEQASLNSL				
Human corona 229E pol 1ab (1746)		RLMKGDGDAEDTLTKLSKYLANEAQVQLEHYSSCCECD				
Murine hepatitis pol 1ab (2004)		GDVVLASDDLYVSRYS	SGCITTFGKPVVWLGHEEASLKS			
Consensus (2029)		GDVVLASDDLYVSRYS	SGCITTFGKPVVWLEHE	ASL	SL	
Section 54						
	(2068)	2068	2080	2090		2106
avian infectious bronchitis pol 1ab (1588)		VLDATSLKATWVEGNANFVVGHPNYYS	-----			
bovine coronavirus pol 1ab (1998)		TYFNRP LLVDENKFDVVKVDDVDGG	-----			
Human corona 229E pol 1ab (1785)		AKFKNSVASLNSAIVCAS	KRDGVQVG	-----		
Murine hepatitis pol 1ab (2043)		TYFNRP SVVCENKFNVL	PVDVSEPTDKGPVPAAVLVTGV			
Consensus (2068)		TYFNRSLLVIENKFNVL	VD	D		

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FIGURE 4A (contd.)

Section 55				
	(2107)	2107	2120	2130 2145
avian infectious bronchitis pol 1ab (1615)	-----	-----	-----	-----KSLHT
bovine coronavirus pol 1ab (2024)	-----	-----	-----	-----DISSDAKES
Human corona 229E pol 1ab (1812)	-----	-----	-----	-----YCVHG
Murine hepatitis pol 1ab (2082)	PGADASAGAGIAKEQKACASASVEDQVVTEVRQEPSVSA			
Consensus (2107)			DI	SVHA
Section 56				
	(2146)	2146	2160	2170 2184
avian infectious bronchitis pol 1ab (1620)	PTFWENAENFVVMGDKIGCVTMGLWRAEHLNKPNIERIF			
bovine coronavirus pol 1ab (2034)	KEINITKLSGVKKPFKVEDSVIVNDDTSEIKYVKSLSTIV			
Human corona 229E pol 1ab (1817)	--IKYYSRVRSVRGRATIVSVEQLEFCAQSRLLSGVAYT			
Murine hepatitis pol 1ab (2121)	ADVKEVKLNGVKKPKVKEGSSVVNDPTSETKVVKSLSTIV			
Consensus (2146)	DIKEIKLNGVKKP	KIEG	SVIVNDPTSESKLVKSLSTIV	
Section 57				
	(2185)	2185	2190	2200 2210 2223
avian infectious bronchitis pol 1ab (1659)	NTAKKALVSSVTTQCGKLGKAAFTFIADKVGGGVVRN			
bovine coronavirus pol 1ab (2073)	DVYDMWLTGCRYVVRTANALSMVNVETTRKFTKFGMTL			
Human corona 229E pol 1ab (1854)	AFSGPVDKCHYTYDTAKKSMYDGDREVKHDLSSLSTIS			
Murine hepatitis pol 1ab (2160)	DVYDMFLTGCKYVWVTANELSRLVNSPTVREYVKWCKGK			
Consensus (2185)	DVYDMFLTGCKYVV	TANKLS	VNSPTIRKVIKFGVT	
Section 58				
	(2224)	2224	2230	2240 2250 2262
avian infectious bronchitis pol 1ab (1698)	ITDSIKGLCGITRG-----			-----HFER
bovine coronavirus pol 1ab (2112)	VSIPIDLLNLREIKPVENN VKAVRNKISACENFIKWLFLV			
Human corona 229E pol 1ab (1893)	VVMVGGYVAPVNTVKKPKPVINQLDEKAQKFFDFGDFLIH			
Murine hepatitis pol 1ab (2199)	IVTPAKLLLRDERQETVAPKVVKAKAIAICYCAVKWFLI			
Consensus (2224)	IVIPIKLL	LRD K	F VIK VK KA ACF	FIKWLL
Section 59				
	(2263)	2263	2270	2280 2290 2301
avian infectious bronchitis pol 1ab (1716)	KMSPOFLKTLMFELFYFLKAS----			VKS-----V
bovine coronavirus pol 1ab (2151)	LLFGWIKRISADNKVIYTTTEVASKLTCKLVALAFKNALLT			
Human corona 229E pol 1ab (1932)	NFVIEFTWLLSMFTLCKTAVTTGDVKIMAKAPORTGVVL			
Murine hepatitis pol 1ab (2238)	YCESWIKENTDNKVIYTTTEVASKLTFKLCCLAFKNALIQ			
Consensus (2263)	LF WIKFSLDNKVIYTTTEVASKLT	KL	LAFKNALLT	
Section 60				
	(2302)	2302	2310	2320 2330 2340
avian infectious bronchitis pol 1ab (1741)	VASYKTVLCKVVLATLLIV	EVYTSNPVMTGIRVLDPL		
bovine coronavirus pol 1ab (2190)	FKWSVVARGACIIATIFDL	FNFIYANVILSDFYLPKIG		
Human corona 229E pol 1ab (1971)	KRSLKYNLKASAAVLKSKW	LLAKETKLLLLIYTLYSVV		
Murine hepatitis pol 1ab (2277)	FNWSVVSRRGFVATVELL	FNFIYANVILSDFYLPNTG		
Consensus (2302)	FKWSVVARGA	IIATIFLLWFNFIYANVILSDFYLP	IG	

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FIGURE 4A (contd.)

Section 61				
	(2341) 2341	2350	2360	2379
avian infectious bronchitis pol 1ab (1780)	FEGLSC	PYKDYG	-----	KDSFDVLR
bovine coronavirus pol 1ab (2229)	FLPTFVCK	AQWIKSTES	LVTTCDLYSI	QDVGFKNQYCN
Human corona 229E pol 1ab (2010)	LLCVRF	---PEN---	ECSETVN---	GYAKSNFVKDDYD
Murine hepatitis pol 1ab (2316)	PLPTFV	QIVAMFKTIE	GVSTICDFYQ	VTDLGYRSSEFN
Consensus (2341)	FLPTFVG	I W KSTF L	TICD Y IKDLGFK	YCN
Section 62				
	(2380) 2380	2390	2400	2418
avian infectious bronchitis pol 1ab (1804)	DDFT RV	LHDKDS	LHLNKHAYS	EQVYKDAASGFI
bovine coronavirus pol 1ab (2268)	GSIACQEL	LAGEFDM	DNYKADV	OYEADRRAFVDYTG
Human corona 229E pol 1ab (2041)	GSLG KM	IFGYQEL	SOFSHDDV	WKHTDPLFSNMQPF
Murine hepatitis pol 1ab (2355)	GSMV	ELCFSGFDM	DNYDATNV	QHVDRRLSFDYISL
Consensus (2380)	GSIICKL	CLAGFDM	LDNYKHIDVVQ	HVIDRRLS DY V
Section 63				
	(2419) 2419	2430	2440	2457
avian infectious bronchitis pol 1ab (1843)	NWLYLVE	LLLFVKPVAG	-----	FVI--ICYCVKYLVLN
bovine coronavirus pol 1ab (2307)	LKIVIELIVS	YALYTAWF	PLFALISIQ	ILTTWLPELFM
Human corona 229E pol 1ab (2080)	LVMVLLIFG	-----	DNYLRCFL	LYEVAOMIS
Murine hepatitis pol 1ab (2394)	FKLVVELV	ICYSLYTVCF	YPLFVLIG	MOLLTTWLPELFM
Consensus (2419)	IKLVLELI	IIGYALYTA	FYPLF LIIIQ	ILTTWLPELFM
Section 64				
	(2458) 2458	2470	2480	2496
avian infectious bronchitis pol 1ab (1874)	STVLQTCVC	TDWEVOTV	FSHFNFMGAG	FYFWLFYKLYT
bovine coronavirus pol 1ab (2346)	LSTLHWSV	RLLVSLANML	PAHVFMREY	ILIASFIKLFIL
Human corona 229E pol 1ab (2107)	TVGVFLG	YKETNWF	LHFIFFDVIC	DELLVTVIVIKVLSF
Murine hepatitis pol 1ab (2433)	LETMHWSAR	LFVEVANML	PAFTLLRFY	IYVMTAMYKVYCL
Consensus (2458)	LSTLHWSV	RLLVWFANML	PAHVILRFY	IYI ALIKVI L
Section 65				
	(2497) 2497	2510	2520	2535
avian infectious bronchitis pol 1ab (1913)	QVHILYC	KDVT EV	KRVARSN	QEVSVV GGRKQIVH
bovine coronavirus pol 1ab (2385)	FRRVAYG	SKPG	LFYKRNRS	SLRVKCSITIGMTRYD
Human corona 229E pol 1ab (2146)	VRHVLEG	ENBD	IAASKSAR	LKFFPVNTIINQVQRFY
Murine hepatitis pol 1ab (2472)	CRHVMYG	SKPG	LFYKRN	SVVVKCSITV GCSLRYD
Consensus (2497)	RHVIYGC	SKPGCL	FCYKRNRS	LRVKVSTIVGGMIRYD
Section 66				
	(2536) 2536	2550	2560	2574
avian infectious bronchitis pol 1ab (1952)	MYTNSGYN	EKKRNWYCRN	CDYGHQ	NFMSPEVAGETS
bovine coronavirus pol 1ab (2424)	VMANGGTG	FCKKHQWNC	IDDSYKPGN	TFTTVEAALDES
Human corona 229E pol 1ab (2185)	VMANG	SKCKKHREF	VD	DSYGYGSIITPEVSR
Murine hepatitis pol 1ab (2511)	VMANG	ETGELTKHQWNC	LN	NSWKPGNTFTTHEAAADLS
Consensus (2536)	VMANGGTG	FCKKHQWNC	INCDSYKPGN	TFTTPEVAADLS

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FIGURE 4A (contd.)

Section 67					
	(2575)	2575	2580	2590	2600
avian infectious bronchitis pol 1ab (1991)		EKT	RRHMKPTAYT	THVVDEACLVDDFVN	KYKAATPGKD
bovine coronavirus pol 1ab (2463)		KEL	RRPTQLDVA	HTVTDVKQVGCYMR	FYERDGGORTY
Human corona 229E pol 1ab (2224)		NIT	TNVQFGPA	VMIDKVEFENGFEYR	LYSCETFWRYN
Murine hepatitis pol 1ab (2550)		KEL	REVNCTDS	YSVTEVKQVGC	SMRLEYERDGGORVY
Consensus (2575)		KEL	RRPVQPTD	AYHTVTEVKQVGC	FMRLFYERDGGOR Y
Section 68					
	(2614)	2614	2620	2630	2640
avian infectious bronchitis pol 1ab (2030)		SASSAVKCF	SVTDFLKKAVFLKEAL	KCEQIS	DGGFIVCN
bovine coronavirus pol 1ab (2502)		DDVNASL	FVDYSNLLHSKVKGV	PNMHVVVE	D-----
Human corona 229E pol 1ab (2263)		FDITESKY	SCKEVPKN---	CNVLD	DFIVFNN G-----
Murine hepatitis pol 1ab (2589)		DDVNASL	FVDMNGLLHSKVKGV	PETHVVVE	E-----
Consensus (2614)		DDVNASL	FVDMS LLHSKVKGV	PD LHVVVVEND	
Section 69					
	(2653)	2653	2660	2670	2680
avian infectious bronchitis pol 1ab (2069)		TQSAHALEEAKN	AIYYA Y	CKETLILDQAT	YEQLVVE
bovine coronavirus pol 1ab (2535)		----	ADKANFLN	AVFYAQS	FRHILMVVDKN
Human corona 229E pol 1ab (2293)		----	TNVTVQVKN	SVYFS L	CRITKLVDS
Murine hepatitis pol 1ab (2622)		----	ADKAGELG	AVEYAJS	YRPMMLMVEKK
Consensus (2653)		----	ADKANFLN	AAVFYAQSL	CRPILMVVDK
Section 70					
	(2692)	2692	2700	2710	2720
avian infectious bronchitis pol 1ab (2108)		PVS	KSVIDKVC	SISSLSISVDTAATN	-----
bovine coronavirus pol 1ab (2570)		TSVTEIT	MEDVYVDTELSMEDV	EKKSINAL	LATAHSSSIKQ
Human corona 229E pol 1ab (2328)		FNG	--VILHKA	YIDVERN	STGK LN-----
Murine hepatitis pol 1ab (2657)		LSVSRT	MEDLYVDSLLNVLDV	RKSLTSFVN	AAHNSLIKE
Consensus (2692)		SVSKT	MEDLYVD	TLLSIFD	VDKKSLNA I AH SIK
Section 71					
	(2731)	2731	2740	2750	2769
avian infectious bronchitis pol 1ab (2134)		-----	YKAGTL	RDALLSITKDEE	AVDMAIFCHN
bovine coronavirus pol 1ab (2609)		GTOTCK	VLDTELS	CARKSCSIDSDVD	TKCLADSVMSAVS
Human corona 229E pol 1ab (2352)		-----	MSLA	ECKRADGLSTSD	HEFTSAISNAHR
Murine hepatitis pol 1ab (2696)		GVOLEQ	VMDTEIG	CARRKCAIDS	SDVETKSTTKSVMSAVN
Consensus (2731)		G QI	VLDTF	ISCARKKCAIDS	SDVDTKBITDSVMSAVN
Section 72					
	(2770)	2770	2780	2790	2808
avian infectious bronchitis pol 1ab (2162)		HDVDY	TGDCFTNVIPS	GIDTGKLT	PRRGFLINADASI
bovine coronavirus pol 1ab (2648)		AGLELT	DES	CNNLVPTYLKG	-DNIVAADLGVLIQNSAKH
Human corona 229E pol 1ab (2380)		CDVLL	SDLSFN	FMSSAKPEEKLS	AYULACCMRAGAKV
Murine hepatitis pol 1ab (2735)		AGVDF	TDES	CNNLVPTIVKS	-DTIVAADLGVLIQNNAKH
Consensus (2770)		AGVDL	TDES	FNNLVPSYK	DKIVAADLGVLIQ AKH

FIGURE 4A (contd.)

Section 73						
	(2809)	2809	2820	2830	2847	
avian infectious bronchitis pol 1ab (2201)		ANLR	KNAP--	PVV	KFSELIKLEDSC	
bovine coronavirus pol 1ab (2686)		VOGN	PAKIAGV	SCIASVDAFNQ	ISDFQHKLKKACCKT	
Human corona 229E pol 1ab (2419)		VNAN	LTKDQTP	IVHAKDFNSLSA	EGRKYIVKTSKAK	
Murine hepatitis pol 1ab (2773)		VOAN	AKAANVACI	SVDAFNQ	SADLOHRLRKACSKT	
Consensus (2809)		VNANVAKAANV	PCISVDAFNQ	LSAD	QKYLRLKAC KTG	
Section 74						
	(2848)	2848	2860	2870	2886	
avian infectious bronchitis pol 1ab (2238)		VREFI	IKSGAKQVI	ACHTQKLLVEKRA	GGIVSGTFKCFK	
bovine coronavirus pol 1ab (2725)		LKCLKL	TYNKQ--	MANVSVLT	TPPSLKGA	
Human corona 229E pol 1ab (2458)		LTPELL	INENQAV	TQTPATSIVAKOGA	DAGH	
Murine hepatitis pol 1ab (2812)		LRIKL	TYNKQ--	EANVPI	LTTPPSLKGA	
Consensus (2848)		LKFKLTYNKQ		VANVPILTTPPSLKAGAVFS		
Section 75						
	(2887)	2887	2900	2910	2925	
avian infectious bronchitis pol 1ab (2277)		SYFKWLL	IFYILET	ACCSGY	YYMEVSKSFVHPMYDVNST	
bovine coronavirus pol 1ab (2755)		-----	YFVYVCELL	SLVCF	IGLWCLMPTTYVHKSDFQ	
Human corona 229E pol 1ab (2490)		-----	SLTNLWLL	CGIVCL	IQFMLCFMPYFMYDIVSS	
Murine hepatitis pol 1ab (2842)		-----	RMLQWLF	EVANL	ICFIVLWALMPTYAVHKSDMQL	
Consensus (2887)			ILYILEFLA	LVCFI	LWLLMPTYHVMYS	
Section 76						
	(2926)	2926	2940	2950	2964	
avian infectious bronchitis pol 1ab (2316)		LHVEGFL	VIDKEVL	REIVPEDT	FSNKKVNDAFWGRPY	
bovine coronavirus pol 1ab (2788)		PVYASY	AVLDN	VLVRDVS	VEDVFA	
Human corona 229E pol 1ab (2523)		FEGYDF	EYIEN	OLKNFE	APLKVRV	
Murine hepatitis pol 1ab (2875)		PLYASE	VIDN	VLRDVS	VTDAFA	
Consensus (2926)		PLYASEFKVIDN	GVLRDVS	VED CFANKFENFDQWYESTF		
Section 77						
	(2965)	2965	2970	2980	2990	3003
avian infectious bronchitis pol 1ab (2355)		DNSRNC	PIVTA	VIDG	DGTVA	TGVP
bovine coronavirus pol 1ab (2827)		GLSYY	NSMA	----	CPIV	VAVVDQ
Human corona 229E pol 1ab (2562)		GFTPL	NK-Q	-----	SCPI	VGVSEI
Murine hepatitis pol 1ab (2914)		GLAYY	RNSKA	----	CPVV	VAVIDQ
Consensus (2965)		GLSYY NSMA		CPIV	VAVGVQ	DIVSTVFENVPT VLR
Section 78						
	(3004)	3004	3010	3020	3030	3042
avian infectious bronchitis pol 1ab (2394)		TQTERK	PWYIPT	WFNREI	VGYYTQ	DSITTEGSEYTSIALF
bovine coronavirus pol 1ab (2862)		YGYHVL	HFI	THALSADG	VQCYTP	HSQTSYSN
Human corona 229E pol 1ab (2594)		VGKTL	IFTL	QAAFGN	AGVCYD	IFGVTTPEK
Murine hepatitis pol 1ab (2949)		YGFHVL	HFI	THAFAT	DSVQCYTP	HMQIPYDN
Consensus (3004)		YGFHVLHFI	THAFANDG	VQCYTPHSQIPY		NEFYASGCVL

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FIGURE 4A (contd.)

Section 79						
	(3043)	3043	3050	3060	3070	3081
avian infectious bronchitis pol 1ab (2433)		SAR	LYLTASNT	POLYCFNGDNDAPGALPFG	TI	PHRV
bovine coronavirus pol 1ab (2901)		SSACTM	FAMADGSPQ	PYCYTEGLMONASLYS	SLV	EHVR
Human corona 229E pol 1ab (2627)		ISA	TRLEGLGCGN	NVYCYNTALMEGSLPYSS	TOANAY	
Murine hepatitis pol 1ab (2988)		SSL	TMLAHADGTPHPYCYT	GGVMHNASLYS	SLA	PHVR
Consensus (3043)		SSACTMLAAADGSPNPYCYTDGLM	NASPYSS	TI	PHVR	
Section 80						
	(3082)	3082	3090	3100	3110	3120
avian infectious bronchitis pol 1ab (2472)		FQPNG	--VRLIVPQQILHTPYV	KFVSDSYCT	GSV	EYT
bovine coronavirus pol 1ab (2940)		NLANAKGFI	RFPFVLRREGLVRI	RTRSMSY	CRVGL	EEA
Human corona 229E pol 1ab (2665)		KYDNGNFI	KLPEVIAQGGFGFRT	RTIATK	CRVGE	VES
Murine hepatitis pol 1ab (3027)		NLAS	SNGVIRFPFVSE	GIVRV	RTRSM	CRVGL
Consensus (3082)		NLANGNGVIRFPEVL	EGIVRV	RTRSMSY	CRVGL	EEA
Section 81						
	(3121)	3121	3130	3140	3159	
avian infectious bronchitis pol 1ab (2509)		RP	YCVSLNPQW	LFNDEYTSKPCVFL	CRSTVRE	MESMV
bovine coronavirus pol 1ab (2979)		DEGIC	FNENGSW	LNNPYRSIPET	CRDVED	IYOLF
Human corona 229E pol 1ab (2704)		NAGV	CEGEDKWE	NDG---	RVANCYV	CRGLWN
Murine hepatitis pol 1ab (3066)		DEGIC	FNENRSW	LNNPYRAMP	TECRNAFD	IHOVL
Consensus (3121)		DEGICFNENKSWVLNNDYRS	SLPGTE	CR	VFDLIF	QIL
Section 82						
	(3160)	3160	3170	3180	3198	
avian infectious bronchitis pol 1ab (2548)		STFFETG	VNPEN	ITYMQLATMFL	LLVVVLE	FAMVE
bovine coronavirus pol 1ab (3018)		KGLAC	PYDELALTASSIAGAILAV	IVVLV	FYYLIK	LKRA
Human corona 229E pol 1ab (2740)		SMFSS	SFSVAAMSGQILLNCALGAF	IFCCFLV	TEFRM	
Murine hepatitis pol 1ab (3105)		GGLVR	PIDIFALTASSVAGAILA	ITVVLAF	YYTI	LKRA
Consensus (3160)		SGLASPVDF	ALTASSIAGAILAV	IVVLIF	YYLIK	LKRA
Section 83						
	(3199)	3199	3210	3220	3237	
avian infectious bronchitis pol 1ab (2586)		KAYAT	TFTITMLVWVI	AFILCVHSYNSV	LAVILLVLY	
bovine coronavirus pol 1ab (3057)		GDYTS	IVFVNVIVWC	VFMMLE	FQVYPTL	SCVYAI
Human corona 229E pol 1ab (2779)		GDLSV	GCTVVVAVLLNNVSYI	NTONLV	PMIAY	AILYE
Murine hepatitis pol 1ab (3144)		GDYTS	VIVNVIVWCIFL	MLF	FQVYPTL	SCLYACEY
Consensus (3199)		FGDYTSIVF	INVIWVCINFL	MLFV	FQVYPTL	SCIYAI
Section 84						
	(3238)	3238	3250	3260	3276	
avian infectious bronchitis pol 1ab (2625)		CYASLV	TSRNTVIMHCWLV	FTFGLTV	PTWLACC	ILGFI
bovine coronavirus pol 1ab (3096)		FYATLY	FPSEISVIMHLOWLV	MYGTIMPL	FFCLLY	ISVV
Human corona 229E pol 1ab (2818)		FATRSLR	--YA-WI	WCAAYLLAYIS	FAWLLCAW	FFLAM
Murine hepatitis pol 1ab (3183)		FYTTL	YFPSEISVVMHLOWLV	MYGATM	PLFCII	VAVV
Consensus (3238)		FYTTL	YFPSEISVIMHLOWLV	MYGSIMPL	WL	LCII

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FIGURE 4A (contd.)

Section 85						
	(3277)	3277	3290	3300	3315	
avian infectious bronchitis pol 1ab (2664)		LYMYTFLFLWCYGT	TKNTRKLYDGN	EFVNYDLAKSL		
bovine coronavirus pol 1ab (3135)		VS-----	NHAFWVFAYCRR	LGTSVRS	DGTFEEMALTTT	
Human corona 229E pol 1ab (2854)		LTGL----	LPSLLKLVSTN	LFEGDKFV	TFESAAGT	
Murine hepatitis pol 1ab (3222)		VS-----	NHALWLFSCYCR	KLGTEVRS	DGTFEEMALTTT	
Consensus (3277)		VS	NHALWL	FKYCRKLGTG	VRSVGTTFEEMALTTT	
Section 86						
	(3316)	3316	3330	3340	3354	
avian infectious bronchitis pol 1ab (2703)		VIRGSEFV	ITNETIG-DKDEA	LSAARLK	YEGTGSEQ	
bovine coronavirus pol 1ab (3168)		MITKDSYCKL	KNSISDVAFNR	ISTLNKYR	YSCKMDTA	
Human corona 229E pol 1ab (2889)		VIDMRSYE	KANSTISPEK	LKSLAAS	NRYKYSGNANE	
Murine hepatitis pol 1ab (3255)		M-TKESYCKL	KNSVSDVAFNR	ELSLNKYR	YSCKMDTA	
Consensus (3316)		MITKDSYCKL	KNSISDV	KFNRYLSLYNKY	KYYSGKMDTA	
Section 87						
	(3355)	3355	3360	3370	3380	3393
avian infectious bronchitis pol 1ab (2741)		DLOLCRAW	LYLDQYR-NSG	VEIVT	PRYSIGV	RI
bovine coronavirus pol 1ab (3207)		AIREACSO	LAKAMDTET	NNNGSDVL	QPETASV	STSEL
Human corona 229E pol 1ab (2928)		DTRCACYA	LAKMLDPS	RDHN-DTL	TPTVSYG	-STL
Murine hepatitis pol 1ab (3294)		AIREACSO	LAKAMETEN	HNNGNDVL	QPETASV	TSTSEL
Consensus (3355)		DYREACCA	QLAKAMDTES	NNG	DILYTPPTAS	VGTSFL
Section 88						
	(3394)	3394	3400	3410	3420	3432
avian infectious bronchitis pol 1ab (2779)		QSGFKALVS	PSSA	PKETVS	VSIRGNN	NGELWLGDTIYC
bovine coronavirus pol 1ab (3246)		QSGIV	MVNPTSK	PTPTVS	VTIGNMT	LNGLWLGDKVYC
Human corona 229E pol 1ab (2965)		QAGLR	MAQPSGF	EKQVVR	CLGNTV	ANGALGIVYC
Murine hepatitis pol 1ab (3333)		QSGIV	MVSTTSK	PTPTVS	VTIGNMT	LNGLWLGDKVYC
Consensus (3394)		QSGIVKMV	SPSSKVEPC	IVSVTYGNMT	LNGLWLGDKVYC	
Section 89						
	(3433)	3433	3440	3450	3460	3471
avian infectious bronchitis pol 1ab (2818)		PRHVLGKF	SGDQWN	VLNLAN	NHEFEV	TTQHC--VTLN
bovine coronavirus pol 1ab (3285)		PRHVIC	SASDMTNPD	YTNLLCR	VTSSDFT	VLFDRLSLTV
Human corona 229E pol 1ab (3004)		PRHVI	ASN-TTSA	INPDHEYS	IMRLHN	ESTTSGTAF
Murine hepatitis pol 1ab (3372)		PRHVIC	SSADMTD	PDYPNLL	CRVTSSD	FCVMGGRMS
Consensus (3433)		PRHVIC	SASDMT	PDY	NLLCRVTSSD	FTVISGRLSLTV
Section 90						
	(3472)	3472	3480	3490	3500	3510
avian infectious bronchitis pol 1ab (2855)		VSRRLK	GAVLILQTA	VAANA	EEAKYKE	IKANCCDSPTIAC
bovine coronavirus pol 1ab (3324)		MSYQM	QGCMLVLT	VTLQNSR	TPKYTE	GVVKPGETFTVLA
Human corona 229E pol 1ab (3042)		VGATMH	GVTEKIK	VSQTMHT	RHSIR	TLKSLGFTNLA
Murine hepatitis pol 1ab (3411)		MSYQM	QGCMLVLT	VTLQNPNT	FKYSFG	VVKPGETFTVLA
Consensus (3472)		MSYQM	QGCMLVLT	VTLQNA	TPKYSE	GVVKPGETFTILA

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FIGURE 4A (contd.)

Section 91																																							
	(3511)	3511	3520	3530	3549																																		
avian infectious bronchitis pol 1ab (2894)	A	G	T	V	V	L	P	V	T	M	R	S	N	G	T	I	R	A	S	F	L	A	A	S	V	G	F	N	I	E	K	G							
bovine coronavirus pol 1ab (3363)	A	N	G	K	P	Q	G	A	F	H	V	T	M	R	S	S	Y	L	I	K	G	S	F	L	C	C	S	G	S	V	G	Y	V	L	M	G	D		
Human corona 229E pol 1ab (3081)	C	D	E	C	A	Q	C	V	E	G	M	M	E	T	N	W	T	I	R	G	S	S	I	N	A	K	P	E	Y	N	L	K	N	G					
Murine hepatitis pol 1ab (3450)	A	N	A	R	P	Q	G	A	F	H	V	T	L	S	S	H	I	K	G	S	F	L	C	S	S	C	S	V	V	V	L	T	G	D					
Consensus (3511)	A	Y	N	G	K	P	Q	G	A	F	H	V	T	M	R	S	S	W	T	I	K	G	S	F	L	C	G	A	C	S	V	G	Y	V	L	G			
Section 92																																							
	(3550)	3550	3560	3570	3588																																		
avian infectious bronchitis pol 1ab (2933)	V	N	F	F	M	H	L	L	P	N	A	L	H	T	G	T	D	L	M	E	E	T	G	Y	V	E	E	N	A	C	R	V							
bovine coronavirus pol 1ab (3402)	C	K	E	V	M	H	O	L	E	I	S	T	G	C	H	T	T	D	F	N	D	F	L	G	P	Y	K	A	Q	V	V	L	P						
Human corona 229E pol 1ab (3120)	E	E	V	N	I	K	O	I	S	G	S	S	H	V	O	S	S	E	D	V	M	I	G	F	E	A	Q	P	N	L	V	E							
Murine hepatitis pol 1ab (3489)	S	R	E	V	M	H	O	L	E	I	S	T	G	C	H	T	T	D	F	S	C	N	E	Y	C	P	Y	R	A	Q	V	V	L	P					
Consensus (3550)	V	K	F	V	M	H	Q	L	E	L	S	T	G	C	H	T	G	T	D	F	G	D	F	G	P	Y	K	D	A	Q	V	V	L	P					
Section 93																																							
	(3589)	3589	3600	3610	3627																																		
avian infectious bronchitis pol 1ab (2972)	P	P	D	N	I	V	T	N	N	T	V	A	W	L	A	A	L	I	S	V	K	E	S	S	F	S	L	P	K	W	L	E	S	T	T	V	S	V	
bovine coronavirus pol 1ab (3441)	V	Q	D	Y	I	Q	S	V	N	F	A	W	L	A	A	I	L	N	N	-----	C	N	W	F	V	Q	S	D	K	C	S	V							
Human corona 229E pol 1ab (3159)	S	A	N	Q	M	L	T	V	V	A	R	E	A	A	T	L	N	G	-----	C	T	W	W	L	K	G	E	K	L	F	V								
Murine hepatitis pol 1ab (3528)	V	Q	D	Y	T	O	T	V	V	A	W	L	A	A	I	L	N	R	-----	C	N	W	F	V	Q	S	D	S	C	S	L								
Consensus (3589)	V	Q	D	Y	I	Q	T	V	N	V	A	W	L	Y	A	A	I	L	N		C	N	W	F	L	Q	S	D	K	C	S	V							
Section 94																																							
	(3628)	3628	3640	3650	3666																																		
avian infectious bronchitis pol 1ab (3011)	D	D	Y	M	K	T	G	D	N	T	T	P	F	S	T	S	T	A	T	T	K	S	A	I	P	S	D	V	C	K	L	R	T						
bovine coronavirus pol 1ab (3474)	E	D	F	N	V	W	A	L	S	N	G	S	Q	V	K	S	D	E	L	V	I	D	A	L	A	S	M	T	G	S	L	E	T	L	A	A	T		
Human corona 229E pol 1ab (3192)	E	H	Y	E	N	Q	A	N	S	T	A	M	N	G	E	D	A	F	S	I	L	A	A	K	T	E	C	V	E	R	L	L	H	A	I				
Murine hepatitis pol 1ab (3561)	E	E	F	N	V	W	A	M	T	N	G	S	S	I	K	A	D	L	V	I	D	A	L	A	S	M	T	G	T	V	E	Q	V	I	A	T			
Consensus (3628)	E	D	F	N	V	W	A	L	S	N	G	F	S	A	I	K	A	D	L	V	I	D	A	L	A	A	M	T	G	V	S	V	E	K	L	L	A	I	
Section 95																																							
	(3667)	3667	3680	3690	3705																																		
avian infectious bronchitis pol 1ab (3050)	M	V	K	N	S	Q	W	G	D	P	D	E	Q	Y	N	F	E	D	E	L	T	P	E	S	V	E	N	I	G	V	R	Q	-						
bovine coronavirus pol 1ab (3513)	K	R	L	K	N	G	F	Q	R	O	T	M	S	C	S	F	E	D	E	L	T	P	S	D	V	Y	Q	L	A	C	I	K	L	C	K				
Human corona 229E pol 1ab (3231)	Q	V	L	N	N	G	E	G	G	K	Q	I	L	G	Y	S	S	L	N	O	E	F	S	I	N	E	V	R	O	M	F	G	V	N	L	O	S		
Murine hepatitis pol 1ab (3600)	K	R	L	H	S	G	F	Q	K	Q	I	L	S	C	V	L	E	D	E	L	T	P	S	D	V	Y	Q	L	A	G	V	K	L	Q	S	K			
Consensus (3667)	K	V	L	N	S	G	F	Q	G	K	Q	I	L	G	S	C	S	L	E	D	E	L	T	P	S	D	V	Y	Q	L	A	G	V	K	L	Q	S	K	
Section 96																																							
	(3706)	3706	3720	3730	3744																																		
avian infectious bronchitis pol 1ab (3088)	-	S	F	V	R	K	A	T	S	-	W	F	W	S	R	C	V	L	A	C	T	L	F	V	L	C	A	I	V	L	F	T	A	V	P	L	K	F	Y
bovine coronavirus pol 1ab (3552)	R	T	R	L	V	K	G	I	V	C	W	I	M	A	S	T	E	L	F	S	C	I	I	T	A	F	V	K	W	T	M	F	Y	V	T	T	N	M	
Human corona 229E pol 1ab (3269)	-	G	K	T	T	S	M	F	K	S	I	S	L	F	A	G	E	F	V	M	E	W	A	E	L	F	V	Y	T	T	T	I	W	V	N	P	G	E	L
Murine hepatitis pol 1ab (3639)	R	T	R	V	I	K	G	T	C	C	W	I	L	A	S	T	F	L	F	C	S	I	I	S	A	E	V	K	W	T	M	F	Y	V	T	T	N	M	
Consensus (3706)	R	T	R	V	I	K	G	T	C	W	I	L	A	S	T	F	L	F	C	F	I	I	S	L	F	V	K	W	T	M	F	Y	V	T	T	N	M		

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FIGURE 4A (contd.)

Section 97							
	(3745)	3745	3750	3760	3770	3783	
avian infectious bronchitis pol 1ab (3125)		VYAAVIL	EMAVL	EFISFTV	IVMAYMDTE	LLPTTITVITIG	
bovine coronavirus pol 1ab (3591)		LSITTF	CAICV	ISLAML	IVIKHLYLT	MYIIEVLFITLLYN	
Human corona 229E pol 1ab (3307)		TPFMILL	VAAESL	CLTFVVR	IKVLF	FLQVFLITSTIVAAIQ	
Murine hepatitis pol 1ab (3678)		EGVTICAL	CFVSE	AMLLIL	IKHLYLT	MYIMEVLCTLFYT	
Consensus (3745)		L	ITICLL	CLVSE	FAMLLV	KHKHLYLTMFILPVLITLIYN	
Section 98							
	(3784)	3784	3790	3800	3810	3822	
avian infectious bronchitis pol 1ab (3164)		VCAEMPF	FIYN	TLLISQ	VVIFLSQ	WYDPVVFDTMVPWMFLP	
bovine coronavirus pol 1ab (3630)		NYLVVYK	QTERG	YVYAW	LSYYV	PSVEYTYTDEVIYGLL	
Human corona 229E pol 1ab (3346)		NCAWDY	HVTKV	LAEKFD	YNVSV	MO	MDIQGFVNIFICLFW
Murine hepatitis pol 1ab (3717)		NYLVVYK	QSPRG	IAYAW	LSHFV	PAVDYTYMDEVIYGVVL	
Consensus (3784)		NYLVVYK	QTERLI	AYAWLS	VSVPA	VDYTY DEVIYGLLL	
Section 99							
	(3823)	3823	3830	3840	3850	3861	
avian infectious bronchitis pol 1ab (3203)		EVLYTA	FKCVQ	GCYMN	SFNTS	LLMLYQFVKLG	FVIYTSS
bovine coronavirus pol 1ab (3669)		ELGMVF	VTLRS	INHD	-----	LFSPIM	FVGRVISV
Human corona 229E pol 1ab (3385)		ALLHTW	RFAKE	R-----	-----	CTHWCT	YLFSLI
Murine hepatitis pol 1ab (3756)		LVAMVF	VTLRS	INHD	-----	VFSIMF	LMGRIVSLV
Consensus (3823)		LVL	MVFV	TTLRS	INHD	LFSEI	LVGRIVSLV
Section 100							
	(3862)	3862	3870	3880	3890	3900	
avian infectious bronchitis pol 1ab (3242)		NTLTAY	TEGNW	EFELV	HTTVL	ANVSSNS	LIGLFVFKC
bovine coronavirus pol 1ab (3699)		SLWYMG	SNLEEE	ILLMI	ASLFG	TYTWT	TALSMAAAKVIA
Human corona 229E pol 1ab (3409)		AVLYTA	LYSYD	YVSL	LVML	CAISNE	WYTGATIFRICRF
Murine hepatitis pol 1ab (3786)		SMWYFG	ANLEEE	VLLFF	TSIFG	TYTWT	TMESDATAKVIA
Consensus (3862)		SLWY	GSNLEEE	VLLLL	MSLFG	TYTWT	TILSIA AKVIA
Section 101							
	(3901)	3901	3910	3920	3939		
avian infectious bronchitis pol 1ab (3281)		AKWMLY	YCNA	TYLNN	YVLM	AVMVN	CIGWLCTC
bovine coronavirus pol 1ab (3738)		KWVAVN	VLYFT	DIPO	KIVL	VCYL	FTGNTIS
Human corona 229E pol 1ab (3448)		GVAFLP	VEYVS	YFDG	VKT	VILFY	MLLEVSCM
Murine hepatitis pol 1ab (3825)		KWLAVN	VLYFT	DVPO	IKLV	LLSY	LCIGYVCC
Consensus (3901)		KWLALN	VLYFT	YIPQ	IKLV	LLYLC	IGYVCCCYWGLLSW
Section 102							
	(3940)	3940	3950	3960	3978		
avian infectious bronchitis pol 1ab (3320)		VMKVFG	LTLG	KYNFK	VSV	DQYR	TMCLHK
bovine coronavirus pol 1ab (3777)		MNSLFR	MPLC	VYNY	KISV	QELR	YMNANGL
Human corona 229E pol 1ab (3487)		LRRECK	CTLC	YVDF	CVPA	EFKY	LVANGL
Murine hepatitis pol 1ab (3864)		LSLFRM	PLCV	YNYK	ISVQ	ELRY	MNANGL
Consensus (3940)		INSIFR	MTLG	VYNFK	ISVQ	ELRY	MNANGLRPPKNSFEAL

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FIGURE 4A (contd.)

Section 103								
	(3979)	3979	3990	4000	4017			
avian infectious bronchitis pol 1ab (3359)		STNILLIQGTEG	DRVLP	PIATV	AKLSVRCTTVVLMQLIT			
bovine coronavirus pol 1ab (3816)		MLNFKLLGIGG	VPIIEVS	QFCSKLT	EVKCANMTLNCLQ			
Human corona 229E pol 1ab (3526)		FLISEKLMELIG	PRTIKVSTV	QSKTTELLCTN	VMGILS			
Murine hepatitis pol 1ab (3903)		MLNFKLLGIGG	VPVIEVS	QLOSRTD	VAIANVVLNCLQ			
Consensus (3979)		MLNFKLLGIGG	VRVIEVSTV	QSKLTDVKCTNV	VLLNCLQ			
Section 104								
	(4018)	4018	4030	4040	4056			
avian infectious bronchitis pol 1ab (3398)		KLNVEANSEMHV	LVEITHK	LASDVGECMDN	ILGMLI			
bovine coronavirus pol 1ab (3855)		HLHVASNSKLW	QCSTL	DELLATS	DLGVAFEKLAQLIT			
Human corona 229E pol 1ab (3565)		NMNIASSTFEWA	CVEMENK	NLCDPETAQELL	LALIA			
Murine hepatitis pol 1ab (3942)		HLHIASNSKLW	QVCSTL	DELLATS	DLGVAFDKLAQLIT			
Consensus (4018)		HLNIASNSKLW	QVCVTLHN	KILATS	DLGVAFDKLLQLLI			
Section 105								
	(4057)	4057	4070	4080	4095			
avian infectious bronchitis pol 1ab (3437)		TLECIDSTID	-----	LSEYCD	DILKRSTVLSVTQERS			
bovine coronavirus pol 1ab (3894)		VLFANPAAVDS	SKCLTS	SIEEVCD	DYAKDN	TVLQALQSEFV		
Human corona 229E pol 1ab (3604)		FFLSKHSDFG	-----	LGDLV	SYFENDS	ILCSVASSTV		
Murine hepatitis pol 1ab (3981)		VLFANPAAVDS	SKCLAS	SIEEVSD	DYVRDNTV	LQALQSEFV		
Consensus (4057)		VLFANPAAVDS	SKCL	SIEEVCD	DYLDKDN	TVLQALQSEFV		
Section 106								
	(4096)	4096	4110	4120	4134			
avian infectious bronchitis pol 1ab (3470)		HLPZYAEYTR	AKNLYEK	VLVD	SKNGGVTOQELAAYRKA			
bovine coronavirus pol 1ab (3933)		NMAAFVHTFV	AKNLD	EARSS	SGSAN---QOLKOLEKAC			
Human corona 229E pol 1ab (3637)		GMPLEVAET	TAROEY	ENAVANG	SS---PDILKQLEKAM			
Murine hepatitis pol 1ab (4020)		NMAAFVE	ELAKNLD	EAKAS	SGSAN---QQQIKOLEKAC			
Consensus (4096)		NMPSEVEYEL	AKKNYDE	ARAS	SGSANQQQIKOLEKAC			
Section 107								
	(4135)	4135	4140	4150	4160	4173		
avian infectious bronchitis pol 1ab (3509)		NIAKSVFED	DLAQK	LDS	ERAMTTMYKFA	VTD	RRRA	
bovine coronavirus pol 1ab (3969)		NIAKSAYE	FDRAAR	BER	DLALT	NMYKFA	RINDKKS	
Human corona 229E pol 1ab (3672)		EVALAEF	DESSQK	INFAEQ	AAAT	TEARAV	NRKS	
Murine hepatitis pol 1ab (4056)		NIAKSAYE	FDRAAR	LERMAD	DLALT	NMYKFA	RINDKKS	
Consensus (4135)		NIAKSAFDR	DRAVQKK	LERMAD	DLALT	NMYKEA	RINDKKS	
Section 108								
	(4174)	4174	4180	4190	4200	4212		
avian infectious bronchitis pol 1ab (3548)		KLVSSALQ	TLLFSL	LKKIL	SEKLN	VLFDO	SSGVV	ELATV
bovine coronavirus pol 1ab (4008)		KVVSALQ	TMLFS	VRKLD	NQALN	SILD	NAVKG	CVPLNAT
Human corona 229E pol 1ab (3711)		KVVSAMH	SLFG	ILRR	MSVDT	ILNMARN	CVPL	SVT
Murine hepatitis pol 1ab (4095)		KVVSALQ	TMLFS	MRKLD	NQALN	SILD	NAVKG	CVPLNAT
Consensus (4174)		KVVSALQ	TLLFSL	MRKLD	NQALN	SILD	NAVKG	VPLNAT

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FIGURE 4A (contd.)

Section 109					
	(4213)	4213	4220	4230	4240 4251
avian infectious bronchitis pol 1ab (3587)		IVCSNR	TLVLPDPETWVKC	VEGVH	TLSTVNNIDTV
bovine coronavirus pol 1ab (4047)		SLAANTLTITIV	FDKSVYDQVVDNV	YVTL	AGNVNQTIT
Human corona 229E pol 1ab (3750)		PATSAARTVVV	VDHDSFVKMMVD	GFVH	AGVNTLQEV
Murine hepatitis pol 1ab (4134)		SLTSNTTITIV	LKOVFDQVVDNV	YVTL	AGNVNHTOFT
Consensus (4213)		PSLSANTLTITIV	PKDVFVQVVDNV	YVTFYAGV	VVWNIQTI
Section 110					
	(4252)	4252	4260	4270	4280 4290
avian infectious bronchitis pol 1ab (3626)		ITAGTELHPTST	GSGLTYCISGAN	IAWPKVNL	TRNGH
bovine coronavirus pol 1ab (4086)		QDSSTTNKQLNE	ISD-----	DCNWP	VLIANRHNE
Human corona 229E pol 1ab (3789)		KINDEKKNVHL	KDVTK-----	ENQEI	VWPLILTCE
Murine hepatitis pol 1ab (4173)		QDADGAVKQLNE	EDV-----	NSTWPE	VIAANRHNE
Consensus (4252)		QDADGTNKQLNE	IS		NNWPLVI LNRHNE
Section 111					
	(4291)	4291	4300	4310	4329
avian infectious bronchitis pol 1ab (3665)		NKVDVVLO	NNELMTHGVKTK	KACVAGVDQAH	CSVESKCY
bovine coronavirus pol 1ab (4116)		VSATVLO	NNELMFAKLKTQ	VVNS-GPDQ	TGNTPTQCY
Human corona 229E pol 1ab (3819)		RVYKIQ	--NNELIFGKMK	VKATKG-EGDGG	ITSEGNAL
Murine hepatitis pol 1ab (4203)		VSTVVLO	NNELMFOKLRTQ	VVNS-GSDMN	CNTPTQCY
Consensus (4291)		VSV VLO	NNELMPAKLKTQ	VVNS G DA	CNTPTQCY
Section 112					
	(4330)	4330	4340	4350	4368
avian infectious bronchitis pol 1ab (3704)		TNISGNSVVA	ITSSNPNL	VASFLEA	ENQTYVDIDP
bovine coronavirus pol 1ab (4153)		NNSNNCKIVY	AILSDVDGLKY	TKILKDD	NFVVLB
Human corona 229E pol 1ab (3855)		NNEGGRAFMY	YVTTKPGM	YVKWEHDS	-VVTVE
Murine hepatitis pol 1ab (4240)		NTTGTGKIVY	AILSDCDGL	YTKIVKED	NCVVLELD
Consensus (4330)		NNSGGGKIVYAIL	SD PGLKYTKILK	DDGN VVLELD	PP
Section 113					
	(4369)	4369	4380	4390	4407
avian infectious bronchitis pol 1ab (3743)		CKFGMKVG	VKVEV	LLMFI	KNTRSI
bovine coronavirus pol 1ab (4192)		CKFTVQD	VKGLKIKY	LFVVG	GNLARGW
Human corona 229E pol 1ab (3893)		CRFVIDT	PTPGQIKY	LFV	NLNNIR
Murine hepatitis pol 1ab (4279)		CKISVOD	VKGLKIKY	LFV	GNLARGW
Consensus (4369)		CKFSVQD	VKGLKIKY	LFV	KNCNTLARGW
Section 114					
	(4408)	4408	4420	4430	4446
avian infectious bronchitis pol 1ab (3782)		LOS	KGHE	TEEVDAVGI	SLCS
bovine coronavirus pol 1ab (4231)		LQAG-TA	TEYASNS	SILSLCA	FAVS
Human corona 229E pol 1ab (3932)		LQAG-KQ	TEFVSNS	HLLTHCS	LA
Murine hepatitis pol 1ab (4318)		LQAG-TA	TEYASNS	SAILSLCA	FAVS
Consensus (4408)		LQAG	TATEYVSNS	SAILSLCAFAV	DPKKTYLDYIKQGG

FIGURE 4A (contd.)

Section 115				
	(4447) 4447	4460	4470	4485
avian infectious bronchitis pol 1ab (3821)	LGNCVKMLTVHNS	SEPAIT	SKPSPTTDCPS	CGASVCL
bovine coronavirus pol 1ab (4269)	PIANMKMLCDHAGT	EMALTVKPDATTN	LSYGGASVCI	
Human corona 229E pol 1ab (3970)	EVGHCKMLTNGS	SSQPTTCTIDSMTT	DTYCGASVCI	
Murine hepatitis pol 1ab (4356)	PVTNCEMLTCDHA	TMLIKREATTNQDS	LEGA	STCTI
Consensus (4447)	PVGNCVKMLTDHAGSGMAITIKPDATTNQDSYGGASVCI			
Section 116				
	(4486) 4486	4500	4510	4524
avian infectious bronchitis pol 1ab (3860)	YCAHIAHFG	GSVGNLGR	QFKSE	DIITTEKDFVGF
bovine coronavirus pol 1ab (4308)	YCARVEHL	----	DVDGLCKLRKE	QVVPVGIKLVS
Human corona 229E pol 1ab (4009)	YCAHVAH	----	TMDLFCQYKEKW	QVPIGTNDPIRE
Murine hepatitis pol 1ab (4395)	YCFSRVEH	----	DVDGLCKLRKE	QVVLGKIKLVS
Consensus (4486)	YCARVEHP		DVDGLCQLKGKQVPIGKDPVSFV	
Section 117				
	(4525) 4525	4530	4540	4550
avian infectious bronchitis pol 1ab (3899)	LRNKVCTVQC	WIGYGC	QDLSLRQPKSSVQSVAGASDF	
bovine coronavirus pol 1ab (4343)	LTNDVCQVCGF	WRDGS	SSVSTD	-----TTVQSKD
Human corona 229E pol 1ab (4044)	LENTCKVCGC	LNHGCTDRT	-----	AIQSF
Murine hepatitis pol 1ab (4430)	LTNDVCQVCGF	WRDGS	SSVGTG	-----SQFQSKD
Consensus (4525)	LTNDVCQVCGFWRDGS	SSCVST		SAIQSKD
Section 118				
	(4564) 4564	4570	4580	4590
avian infectious bronchitis pol 1ab (3938)	KNYLNRVTCSS	-EARLIPLAS	CDPQVVKEL	EDVCKNES
bovine coronavirus pol 1ab (4373)	TNFLNRVTCSS	-ESTVDARLVPCAS	GLDTHVOL	AFEDICASV
Human corona 229E pol 1ab (4072)	NSYLNRVTCSS	-SARLEPCNETDIDYCV	ATPVYKDA	
Murine hepatitis pol 1ab (4460)	TNFLNRVTCSS	-SVNARLVPCAS	GLDTHVOL	AFEDICANR
Consensus (4564)	TNFLNRVRGSSVDARLVPCASGLDTHVOLAFEDICNKDA			
Section 119				
	(4603) 4603	4610	4620	4630
avian infectious bronchitis pol 1ab (3976)	AGMFQNLARMCA	ETQELRDTEDGNLEYL	SSYFV	QOTTP
bovine coronavirus pol 1ab (4412)	AGIGLHL	VNCCRFQRVDE	NGD	----KLQFFV
Human corona 229E pol 1ab (4109)	SFTGKNL	SSVNRKNVDKD	-----	AFYI
Murine hepatitis pol 1ab (4499)	AGIGLYYV	NCCRFQRVDE	NGD	----KLKFFV
Consensus (4603)	AGIGLNLKVNCCRFQRVDE	NGD		KLDAFFVVKRT L
Section 120				
	(4642) 4642	4650	4660	4670
avian infectious bronchitis pol 1ab (4015)	SNYEHEKSC	LEDLS	-EVTADLDE	EVFNKN
bovine coronavirus pol 1ab (4447)	TIYNREMECY	ERVNDCKEVA	EHD	FTTFDVEGSRVPHIV
Human corona 229E pol 1ab (4140)	SVMDH	QSMYLL	GCNAVAKHDI	ETWHEGRTIYGNVSE
Murine hepatitis pol 1ab (4534)	EVYNKEKEC	YELTECGVVA	EHEE	FTEDVEGSRVPHIV
Consensus (4642)	SVYNHEKSCYELLKDC	VVAEHDF	FTTFDVEGSRVPHIV	

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FIGURE 4A (contd.)

Section 121				
	(4681) 4681	4690	4700	4719
avian infectious bronchitis pol 1ab (4050)	QRRTKYTMMLFCYALRHFPKDC	EVLRKEILVTYGCIEDY		
bovine coronavirus pol 1ab (4486)	KDLTKYTMMLFCYALRHFPKDC	EVLRKEILVTYGCIEDY		
Human corona 229E pol 1ab (4179)	QDLTKYTMMLFCYALRHFPKDC	EVLRKEILVTYGCIEDY		
Murine hepatitis pol 1ab (4573)	KDLTKYTMMLFCYALRHFPKDC	EVLRKEILVTYGCIEDY		
Consensus (4681)	QDLTKYTMMLFCYALRHFPKDC	EVLRKEILVTYGCIEDY		
Section 122				
	(4720) 4720	4730	4740	4758
avian infectious bronchitis pol 1ab (4089)	HPKWFEENRDLVYDPTIENSKYYV	MLAKMPTVRR	ELNAT	
bovine coronavirus pol 1ab (4525)	Y----	FTKIDLYDFVENRDTINVKKL	PIFNR	LVSAT
Human corona 229E pol 1ab (4218)	Y----	FEMINFCPTFEDIHRVYAAL	KVVAN	MLKCV
Murine hepatitis pol 1ab (4612)	Y----	EOKDLYDFVENRDTINVKKL	PIFNR	LINTA
Consensus (4720)	Y	FEKKDWYDPIENPDIINVKKL	GPIVNRALLNAT	
Section 123				
	(4759) 4759	4770	4780	4797
avian infectious bronchitis pol 1ab (4128)	EEGNLMYEKLYCVTHDNDLNGKF	DEGDFQKTARCA		
bovine coronavirus pol 1ab (4560)	EEADKL	EVLLVGLVLTLDNQLNGKF	YDFVIAAPLC	
Human corona 229E pol 1ab (4253)	ACDEM	LLKVVGLVLTLDNQLNGKF	YDFVLCPECM	
Murine hepatitis pol 1ab (4647)	KFADAL	EAELVGLVLTLDNQLNGKF	YDFVKTVEGC	
Consensus (4759)	EEFAD	LVEKGLVGLVLTLDNQLNGKF	YDFGDFVKTAPGC	
Section 124				
	(4798) 4798	4810	4820	4836
avian infectious bronchitis pol 1ab (4167)	GVPVFDTYEYMPITAMTDAAP	RYFEYD	VHKGYS	
bovine coronavirus pol 1ab (4599)	GVATADSYEYMPMLTCHADCE	LYVN	-----	NAYRL
Human corona 229E pol 1ab (4292)	CTPYCTSYEYMPVMGTNCHAS	CFMKSDIFG	QDFKT	
Murine hepatitis pol 1ab (4686)	GVAVADSYEYMPMLTCHADCE	LYVN	-----	GTyre
Consensus (4798)	GVPVADSYEYMPMLTMTHALD	SELFVN	D	NAYKS
Section 125				
	(4837) 4837	4850	4860	4875
avian infectious bronchitis pol 1ab (4205)	YDLKLYDYTEERQELIQYENY	DQE	APNCRD	SDDR
bovine coronavirus pol 1ab (4633)	FELVQIDFDYLLFENYTHH	SMP	TNTVDC	QDDRC
Human corona 229E pol 1ab (4331)	FDLKLDTEHKEVLIN	YENY	QOD	HPDCVDEHDEM
Murine hepatitis pol 1ab (4720)	FELVQIDFDYLLFENYTHH	SMT	TNTCE	ELDR
Consensus (4837)	FDLLQYDFTDHLKLELFNKYFK	HWSQDYHPNTVDC	DDRC	
Section 126				
	(4876) 4876	4890	4900	4914
avian infectious bronchitis pol 1ab (4244)	LIHCANFNILFSTVLPNTCEG	PLVRQIFVDGVPFVVSIG		
bovine coronavirus pol 1ab (4672)	LIHCANFNILFSTVLPNTCEG	PLVRQIFVDGVPFVVSIG		
Human corona 229E pol 1ab (4370)	LIHCANFNILFSTVLPNTCEG	PLVRQIFVDGVPFVVSIG		
Murine hepatitis pol 1ab (4759)	LIHCANFNILFSTVLPNTCEG	PLVRQIFVDGVPFVVSIG		
Consensus (4876)	LIHCANFNILFSTVLPNTCEG	PLVRQIFVDGVPFVVSIG		

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FIGURE 4A (contd.)

Section 127						
	(4915)	4915	4920	4930	4940	4953
avian infectious bronchitis pol 1ab (4283)		YHS	ELGVIM	QNTMSFSKMGLSQIMQFVGL	AL	LT
bovine coronavirus pol 1ab (4711)		YHY	ELGVIM	MDVDTHRYRLSLKD	LLYAA	ALHVAS
Human corona 229E pol 1ab (4409)		YHE	QGLVW	NKLVNTHSTRLLTITELLQFVT	ET	TIAS
Murine hepatitis pol 1ab (4798)		YHY	ELGVIM	MDVDTHRYRLSLKD	LLYAA	ALHVAS
Consensus (4915)		YHY	KELGVVMNMDVDTHRYRLSLKD	LLQFVADPALHVAS		
Section 128						
	(4954)	4954	4960	4970	4980	4992
avian infectious bronchitis pol 1ab (4322)		SNNTV	DLPLS	ICALTS	LITH	CHHFNKD
bovine coronavirus pol 1ab (4750)		ASALYDLRTCCFS	VAAITSGVKE	QTVKPNF	QOD	FT
Human corona 229E pol 1ab (4448)		SPA	VLEK	TVGLVAALST	LLTSQIV	PHHKE
Murine hepatitis pol 1ab (4837)		ASALYDLRTCCFS	VAAITSGVKE	QTVKPNF	QOD	FT
Consensus (4954)		ASALV	DLRTCCFSVAAITSGVTE	FQTVKPGNFN	QDFYDFI	
Section 129						
	(4993)	4993	5000	5010	5020	5031
avian infectious bronchitis pol 1ab (4361)		EKA	MFKEG	SIP	NNH	YPOTENAA
bovine coronavirus pol 1ab (4789)		LSK	LLKEG	SSVD	LFHFTQD	NAATLYN
Human corona 229E pol 1ab (4487)		RSQ	FFDEG	SEET	YK	FTOKED
Murine hepatitis pol 1ab (4876)		LSK	LLKEG	SSVD	LFHFTQD	NAATLYN
Consensus (4993)		LSKGLL	KEGSSVDLKHFFFTQDGNAAITDYN	YKYNRPT		
Section 130						
	(5032)	5032	5040	5050	5060	5070
avian infectious bronchitis pol 1ab (4400)		MFD	COLLFCLE	TSK	TECEGGCIPASQ	VNNLDK
bovine coronavirus pol 1ab (4828)		MVDIKQLLFVLE	VVAKYFEI	YEGGCIPASQ	TNNYD	KS
Human corona 229E pol 1ab (4526)		LLIG	QARVAYQ	AAARFDC	EEG	CTSRENVVT
Murine hepatitis pol 1ab (4915)		MVDIKQLLFVLE	VVAKYFEI	YEGGCIPASQ	TNNYD	KS
Consensus (5032)		MVDIKQLLFVLE	VVAKYFEIYEGGCIPASQ	VIVNNYD	KS	
Section 131						
	(5071)	5071	5080	5090	5109	
avian infectious bronchitis pol 1ab (4439)		AGYFF	NTFGKARLY	YEALS	FEEQDEIFAYTKRNVLP	TLT
bovine coronavirus pol 1ab (4867)		AGYFF	NTFGKARLY	YEALS	FEEQDEIFAYTKRNVLP	TLT
Human corona 229E pol 1ab (4565)		AGYFF	NTFGKARLY	YEALS	FEEQDEIFAYTKRNVLP	TLT
Murine hepatitis pol 1ab (4954)		AGYFF	NTFGKARLY	YEALS	FEEQDEIFAYTKRNVLP	TLT
Consensus (5071)		AGYFF	NKFGKARLYYEALS	FEEQDEIFAYTKRNVLP	TLT	
Section 132						
	(5110)	5110	5120	5130	5148	
avian infectious bronchitis pol 1ab (4477)		QMN	LKYAISAKNRARTVAGV	SILSTMTGRQFHQCKL	KS	
bovine coronavirus pol 1ab (4906)		QMN	LKYAISAKNRARTVAGV	SILSTMTGRQFHQCKL	KS	
Human corona 229E pol 1ab (4604)		QMN	LKYAISAKNRARTVAGV	SILSTMTGRQFHQCKL	KS	
Murine hepatitis pol 1ab (4993)		QMN	LKYAISAKNRARTVAGV	SILSTMTGRQFHQCKL	KS	
Consensus (5110)		QMN	LKYAISAKNRARTVAGV	SILSTMTGRQFHQCKL	KS	

FIGURE 4A (contd.)

Section 133				
	(5149)	5149	5160	5170 5187
avian infectious bronchitis pol 1ab (4516)	VNTRNASV	VLGLTFFYGGW	DNMLRNI	IQGVEDPIHMGWD
bovine coronavirus pol 1ab (4945)	AATFGVBY	VTETPKAYGG	LDLRRLEIKD	DNEVVLGWD
Human corona 229E pol 1ab (4643)	VATFNATTA	ELTTFYGG	INLKNLMAD	VDDPKELMGWD
Murine hepatitis pol 1ab (5032)	AATAGVP	VLGLTFFYGG	WDDMRR	LKDIDSEVIMCWD
Consensus (5149)	VATRNVPV	VIGTTKFYGG	WDNMLRRL	LKDVDDPVLIMGWD
Section 134				
	(5188)	5188	5200	5210 5226
avian infectious bronchitis pol 1ab (4555)	YPKCDRA	PNLLTAAS	LVITAR	ITNEGQSWSERI
bovine coronavirus pol 1ab (4984)	YPKCDRA	PNLLIRIV	SSLVLAR	HEACTSQSDRF
Human corona 229E pol 1ab (4682)	YPKCDRA	PNLLSMT	MLSAMT	IGSLVTTG
Murine hepatitis pol 1ab (5071)	YPKCDRA	PNLLIRIV	SSLVLAR	ITDSCSHTDRE
Consensus (5188)	YPKCDRA	PNLLIRIV	SSLVLARK	HDSCSSDRFYRLAN
Section 135				
	(5227)	5227	5240	5250 5265
avian infectious bronchitis pol 1ab (4594)	ECAQVLS	EIVMCGG	GYVVKP	GGTSSGDATTAY
bovine coronavirus pol 1ab (5023)	ECAQVLS	EIVMCGG	GYVVKP	GGTSSGDATTAF
Human corona 229E pol 1ab (4721)	ECAQVLS	EIVMCGG	GYVVKP	GGTSSGDATTAY
Murine hepatitis pol 1ab (5110)	ECAQVLS	EIVMCGG	GYVVKP	GGTSSGDATTAF
Consensus (5227)	ECAQVLS	EIVMCGG	GYVVKP	GGTSSGDATTAFANSVFN
Section 136				
	(5266)	5266	5280	5290 5304
avian infectious bronchitis pol 1ab (4633)	IQATSA	IVARLLSV	ITRDLVYD	NIKSLCYEL
bovine coronavirus pol 1ab (5062)	CQAVS	ANVCAL	MSCN	GNKIEDLSIR
Human corona 229E pol 1ab (4760)	CQAVS	ANVCAL	MSCN	GNKIEDLSIR
Murine hepatitis pol 1ab (5149)	CQAVS	ANVCAL	MSCN	GNKIEDLSIR
Consensus (5266)	CQAVS	ANVCALLSVN	GKIEDLSIKALQ	KRLYSNVYRAD
Section 137				
	(5305)	5305	5310	5320 5330 5343
avian infectious bronchitis pol 1ab (4672)	NVDPAF	VSEFYE	FLNKH	FMSMILSDDG
bovine coronavirus pol 1ab (5101)	NVDPAF	VSEFYE	FLNKH	FMSMILSDDG
Human corona 229E pol 1ab (4799)	NVDPAF	VSEFYE	FLNKH	FMSMILSDDG
Murine hepatitis pol 1ab (5188)	NVDPAF	VSEFYE	FLNKH	FMSMILSDDG
Consensus (5305)	NVDPAF	VSEFYE	FLNKH	FMSMILSDDGVVCYNSTYASKG
Section 138				
	(5344)	5344	5350	5360 5370 5382
avian infectious bronchitis pol 1ab (4711)	LVADT	SGIREV	LYQNN	VFADSTCN
bovine coronavirus pol 1ab (5140)	YIANE	SAFQQV	LYQNN	VFADSTCN
Human corona 229E pol 1ab (4838)	YIANE	SAFQQV	LYQNN	VFADSTCN
Murine hepatitis pol 1ab (5227)	YIANE	SAFQQV	LYQNN	VFADSTCN
Consensus (5344)	YIANE	SAFQQV	LYQNN	VFADSTCN

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FIGURE 4A (contd.)

Section 139					
	(5383)	5383	5390	5400	5410 5421
avian infectious bronchitis pol 1ab (4750)		SQHTMLVEVDGEPKTEEFED	SRILIG	CVPVIVDVIDTEP	
bovine coronavirus pol 1ab (5179)		SQHTMLVKMDGDDVYLPEELLSRILIG	GCFVDDLLK	DS	
Human corona 229E pol 1ab (4877)		SQHTMQIVDENGKYLPFTBPR	ISAGVVDLITE	DA	
Murine hepatitis pol 1ab (5266)		SQHTMLVKMDGDEVILPEELLSRILIG	GCFVDDLLK	DS	
Consensus (5383)		SQHTMLVKMDGDDVYLPYDP	SRILGAGVFVDDLLK	DS	
Section 140					
	(5422)	5422	5430	5440	5450 5460
avian infectious bronchitis pol 1ab (4789)		VAVMMYIATATE	NYPIVHIENEENKKY	TFVL	AYIRKK
bovine coronavirus pol 1ab (5218)		VLLIERFVSL	YVYHENE	QOK	FRVYLEYIKK
Human corona 229E pol 1ab (4916)		VLLIRYVSL	ALAAFLSKHPKP	RR	YALIDWVKHL
Murine hepatitis pol 1ab (5305)		VLLIERFVSL	YVYHENE	QNYR	FRVYLEYIKK
Consensus (5422)		VLLIERFVSLAIDAYPLVYH	ENPEYQK	VERVYLEYIKK	
Section 141					
	(5461)	5461	5470	5480	5499
avian infectious bronchitis pol 1ab (4828)		YQELSONMIMDY	EFVMDIDKGS	IWEQEL	ENMRAPTT
bovine coronavirus pol 1ab (5257)		YNDLGNQILDSY	VILSTCDGQ	ETDEST	KNMYLRSAV
Human corona 229E pol 1ab (4955)		NKTINEGM	ESFVTLDEHES	KEWDES	ASLEKSTV
Murine hepatitis pol 1ab (5344)		YNDLGNQILDSY	VILSTCDGQ	ETDEST	KNMYLRSAV
Consensus (5461)		YNDLGNQILDSYSVILSTCDG	SKFWEDES	FYKNMYLRSTV	
Section 142					
	(5500)	5500	5510	5520	5538
avian infectious bronchitis pol 1ab (4867)		LQSCVEHNS	STIRQANOTEKEF	LOCC	COYTHVMT
bovine coronavirus pol 1ab (5296)		MDSV	ACNFS	SCSSESGSLIK	KLCCCOYTHVMT
Human corona 229E pol 1ab (4994)		LQAAPL	ENMGQIVLR	QEDCL	RIMLTCAEDHVFGT
Murine hepatitis pol 1ab (5383)		LQSVGAC	VCSST	SLQCSST	IKPLLCCKAATHVMT
Consensus (5500)		LQSVGACVVCSSQTS	SLRCGSCIRKPL	LCCKCCYDHVMT	
Section 143					
	(5539)	5539	5550	5560	5577
avian infectious bronchitis pol 1ab (4906)		PHHNV	SINF	ICSQLOCGEA	VIATATGMSYFCGNIE
bovine coronavirus pol 1ab (5335)		PHKYVLSV	SPVGNAPG	LDVND	TATATGMSYFCEDH
Human corona 229E pol 1ab (5033)		PHKFL	ATTE	VCNTS	ENVNDIKVTLALNICYVDHE
Murine hepatitis pol 1ab (5422)		PHKYVLSV	SPVNSPGCDVND	VTKLYLGMSYFCEDH	
Consensus (5539)		PHKYVLSISPYVCNS	PGCDVNDVTKLYLGMSYFCEDH		
Section 144					
	(5578)	5578	5590	5600	5616
avian infectious bronchitis pol 1ab (4945)		PKLGIP	LVSNCT	ITCIYRANCA	SENVDDFNOLATTNWS
bovine coronavirus pol 1ab (5374)		PQYSFK	LVNMEN	VEGLYKQSC	TGSPYIDDEKRIASCKWT
Human corona 229E pol 1ab (5072)		PHLEFP	CSAGNV	EGLYKSSAL	EMDIDVTKLISTSDWS
Murine hepatitis pol 1ab (5461)		PQYSFK	LVNMEN	VEGLYKQSC	TGSPYIDDEKRIASCKWT
Consensus (5578)		PQYSFPLVSN	GMVFGLYKQSC	TGSPYIDDEKRIASCKWS	

FIGURE 4A (contd.)

Section 145					
	(5617) 5617	5630	5640	5655	
avian infectious bronchitis pol 1ab (4984)	IVEPILANRCSDSIRRLAAETVKAETHELHQQFASAEV				
bovine coronavirus pol 1ab (5413)	DVDDYILANECTERIKLEAATQATYAFKQSYASATI				
Human corona 229E pol 1ab (5111)	DIRDKLANDAKESTRLEAETVKAETSVISSYAYTLE				
Murine hepatitis pol 1ab (5500)	EVDDVILANECTERIKLEAATQATEAFKQCYASATI				
Consensus (5617)	DVDDYILANECTESLKLFAAETVKATEEAFKQSYASATI				
Section 146					
	(5656) 5656	5670	5680	5694	
avian infectious bronchitis pol 1ab (5023)	REIVFSDRRLILSLTPGETREELIRRYFTGYHETRTSKV				
bovine coronavirus pol 1ab (5452)	QELVSRRLILSWEIGAVKALLNKNYVFTGYHETKNGKT				
Human corona 229E pol 1ab (5150)	KEIVGPKRLILLSSQAKALNRNSVFCQIHKDSNF				
Murine hepatitis pol 1ab (5539)	REIVSDRELILSWEIGAVRPLNKNYVFTGYHETKNGKT				
Consensus (5656)	REIVSDRELILSWEIGKVKPPLNKNYVFTGYHETKNSKT				
Section 147					
	(5695) 5695	5700	5710	5720	5733
avian infectious bronchitis pol 1ab (5062)	QLGDFTEFEGEGKDV-VYKATSTALTSVCDIFVLTHN				
bovine coronavirus pol 1ab (5491)	VLGEYVVDSELING-VYRATTTYKLSVDVFLTSHS				
Human corona 229E pol 1ab (5189)	QVGEFVENVVDYGSDTCTKSTATTTLVPEMLILLEHN				
Murine hepatitis pol 1ab (5578)	VLGEYVVDSELING-VYRATTTYKLSVCDVFTIDERHA				
Consensus (5695)	VLGEFVFDKSELING VYKATTTYKLSVGDVFILTSHN				
Section 148					
	(5734) 5734	5740	5750	5760	5772
avian infectious bronchitis pol 1ab (5100)	VVSLVAPTLCPQOTFSRFVNLRPNVMPCCFVINIPLTH				
bovine coronavirus pol 1ab (5529)	VANLSAPTLVPQE-NYSSIRFASVYSLETFOINVVNQ				
Human corona 229E pol 1ab (5228)	VAPRLTLMANCKYSTIYKIHPSENVSDAYANLVPYQ				
Murine hepatitis pol 1ab (5616)	VSSLSAPTLVPQE-NYTSIRFASVYSPLETFOINVPNQ				
Consensus (5734)	VASLSAPTLVPQE NYTSIRLASVYSVPETFOQNNVPNYQ				
Section 149					
	(5773) 5773	5780	5790	5800	5811
avian infectious bronchitis pol 1ab (5139)	LVCKOKRTLVGGPDSKQHFALGLAVYFSSAVVFTAC				
bovine coronavirus pol 1ab (5567)	HIGMKRYCLVGGPDSKSHLAIGLAVYCTARVVFTAA				
Human corona 229E pol 1ab (5267)	LIGKQRITTIIDGSGKSHCSIGIGVYPGAPLFTAC				
Murine hepatitis pol 1ab (5654)	HIGMKRYCLVGGPDSKSHLAIGLAVYCTARVVFTAA				
Consensus (5773)	LIGMQRYTTVQGPPGSGKSHLAIGLAVYYCTARVVFTAC				
Section 150					
	(5812) 5812	5820	5830	5840	5850
avian infectious bronchitis pol 1ab (5178)	SHAAVDALCEKAHKFLKVDCTRIVPQRTTDCFSKFKA				
bovine coronavirus pol 1ab (5606)	SHAAVDALCEKAHKFLNINDCTRIVLAKVRVDCYDKFKI				
Human corona 229E pol 1ab (5306)	SHAAVDSLCATVTAYSVDKCTRTITARARVDCYSGKAP				
Murine hepatitis pol 1ab (5693)	SHAAVDALCEKAHKFLNINDCTRIVLAKVRVDCYDKFKI				
Consensus (5812)	SHAAVDALCEKAHKFLNINDCTRIVPAKVRVDCYSKFKI				

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FIGURE 4A (contd.)

Section 151					
	(5851)	5851	5860	5870	5889
avian infectious bronchitis pol 1ab (5217)	NDTGKK	INSTIPALH	AVSCDILLML	Y	SMITNLE
bovine coronavirus pol 1ab (5645)	NDTTRKY	VFTTIN	ALPEMVT	DIVV	DLV
Human corona 229E pol 1ab (5345)	NNNSAQ	IVSEIV	NALPEVN	ADIVV	DM
Murine hepatitis pol 1ab (5732)	NDTTRKY	VFTTIN	ALPEMVT	DIVV	DLV
Consensus (5851)	NDTTRKY	VFTTIN	ALPEVVT	DIVVV	DEVSM
Section 152					
	(5890)	5890	5900	5910	5928
avian infectious bronchitis pol 1ab (5256)	NGKINY	QYVV	V	EDPAQ	EL
bovine coronavirus pol 1ab (5684)	NARTRAKHY	Y	IGDPA	QLP	APRVLL
Human corona 229E pol 1ab (5384)	NORISYKH	HY	YIGDPA	QLP	APRVLL
Murine hepatitis pol 1ab (5771)	NSRVS	AKHY	YIGDPA	QLP	APRVLL
Consensus (5890)	NARISYKH	Y	YIGDPA	QLP	APRVLL
Section 153					
	(5929)	5929	5940	5950	5967
avian infectious bronchitis pol 1ab (5294)	NLMVCVK	EDIFL	AKCY	KE	KEID
bovine coronavirus pol 1ab (5723)	KLMCC	LGPDIF	LGTC	YR	CPKEI
Human corona 229E pol 1ab (5423)	QR	CAIG	PDV	THK	CPKEI
Murine hepatitis pol 1ab (5810)	KLMCC	LGPDIF	LGTC	YR	CPKEI
Consensus (5929)	KLMCC	LGPDIF	LGTC	YR	CPKEI
Section 154					
	(5968)	5968	5980	5990	6006
avian infectious bronchitis pol 1ab (5333)	PE	RE	EF	VI	VN
bovine coronavirus pol 1ab (5762)	ES	SL	CF	KV	YK
Human corona 229E pol 1ab (5462)	EA	KQ	EF	LI	FERG
Murine hepatitis pol 1ab (5849)	DN	SM	CF	KV	YK
Consensus (5968)	EASSL	CFKV	YK		
Section 155					
	(6007)	6007	6020	6030	6045
avian infectious bronchitis pol 1ab (5372)	R	KQ	RE	EF	VI
bovine coronavirus pol 1ab (5798)	AN	PL	HK	AV	FI
Human corona 229E pol 1ab (5498)	K	N	ST	SK	AV
Murine hepatitis pol 1ab (5885)	AN	P	S	W	S
Consensus (6007)	AN	P	S	W	S
Section 156					
	(6046)	6046	6060	6070	6084
avian infectious bronchitis pol 1ab (5411)	YDY	V	EC	VT	AD
bovine coronavirus pol 1ab (5837)	YDY	V	EC	VT	AD
Human corona 229E pol 1ab (5537)	YDY	V	EC	VT	AD
Murine hepatitis pol 1ab (5924)	YDY	V	EC	VT	AD
Consensus (6046)	YDY	V	EC	VT	AD

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FIGURE 4A (contd.)

Section 157						
	(6085)	6085	6090	6100	6110	6123
avian infectious bronchitis pol 1ab (5450)		DELYSALKFTELDSETS	-----	LOGTGEPN	ICNKEFS	
bovine coronavirus pol 1ab (5876)		QLEFALQFTTLTLDKVPQAVETRVOCSTNLEKDCSKSYS				
Human corona 229E pol 1ab (5576)		TLEDALKFFEITMTDLQ	-----	SESS-CGLTKD	ARNPI	
Murine hepatitis pol 1ab (5963)		QLFESLNFTTLTLDKIN	---	NPRLOCTTN	LD	SRSYV
Consensus (6085)		QLFEALNFTTLTLDKIN			RLQCSTNLEKDCSKSYS	
Section 158						
	(6124)	6124	6130	6140	6150	6162
avian infectious bronchitis pol 1ab (5482)		GVHPAYAVTTKALAATYLVNDELAALVNVEAGSEITPKH				
bovine coronavirus pol 1ab (5915)		GYHPAHAPSEFLAVDDKYKATGDLAVCLGIGDS-AVITYSR				
Human corona 229E pol 1ab (5609)		DLPESHATTYLSLSDRFETSGD		VOIGNNN--	VCLREH	
Murine hepatitis pol 1ab (5999)		GYHPAHAPSEFLAVDDKYKVGDLAVCLNVADS-AVITYSR				
Consensus (6124)		GYHPAHAPSEFLALDDKYKVSGLAVCLNVADS			AVITYSR	
Section 159						
	(6163)	6163	6170	6180	6190	6201
avian infectious bronchitis pol 1ab (5521)		LISLLSKMSVNVEECHNMFTTRDEAIRNPGVGFIV				
bovine coronavirus pol 1ab (5953)		LTSLMGFKLDVLTLDYCKLELIKKEAVKRPAAVCEIAF				
Human corona 229E pol 1ab (5646)		VTEYMGTRFDVSMPSHSLCIRDFAMRHAGLEMDV				
Murine hepatitis pol 1ab (6037)		LTSLMGFKLDLTLDYCKLEITRDEIKRVRAVCEIAF				
Consensus (6163)		LISLMGFKLDVTLDDGYHKLFIITRDEAIKRVRAWVGFDVE				
Section 160						
	(6202)	6202	6210	6220	6230	6240
avian infectious bronchitis pol 1ab (5560)		ATHACGTNLSTNLPFFVCFSTCAAVVTEEGLYVDTSIGN				
bovine coronavirus pol 1ab (5992)		GAHATRDSIGTNEFLQLGSTTGLVVEATLFAERDCY				
Human corona 229E pol 1ab (5685)		GAHVGGDNVCTNVELVGFENVTEAGPECVLTNTGS				
Murine hepatitis pol 1ab (6076)		GAHATRDSIGTNEFLQLGSTTGLVVEATMFAERDCY				
Consensus (6202)		GAHATRDSIGTNEFLQLGFSTGIDFVVEPTGLVATRDCY				
Section 161						
	(6241)	6241	6250	6260	6279	
avian infectious bronchitis pol 1ab (5599)		NFEFVNSKAFAGLQENLIRVVEFKSAKPHHTIPPVQML				
bovine coronavirus pol 1ab (6031)		SEFKKAVAKAPPGGEQFKHLIPLMTRGQRDAVVPATVQNF				
Human corona 229E pol 1ab (5724)		VVKFVRARAPPGGQTHIVPLLRKGQPSLKKAVQMI				
Murine hepatitis pol 1ab (6115)		VFKKAAARAPPGGEQFKHLIPLMSRGQKWDVVRIPVQML				
Consensus (6241)		VFKFPVAKAPPGGEQFKHLIPLMSRGQPDVVRIPVQML				
Section 162						
	(6280)	6280	6290	6300	6318	
avian infectious bronchitis pol 1ab (5638)		ADNLCMVSLCVVFTWCHGDELTTLRYFVKIGREVCCV				
bovine coronavirus pol 1ab (6070)		ADHLLIDLSICVVLVTWAANFELTCLRYFAKVGREVSQV				
Human corona 229E pol 1ab (5763)		ADFLAGSSIVLFTWAGGLELTTLRYFAKVGREVSQV				
Murine hepatitis pol 1ab (6154)		SDHLADLANSVLTWAASELTCLRYFAKVGREVSQV				
Consensus (6280)		ADHLADLSDCVVLVTWAAGLELTTLRYFVKIGREVCCV				

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FIGURE 4A (contd.)

Section 163				
	(6319) 6319	6330	6340	6357
avian infectious bronchitis pol 1ab (5676)	NGSR	ITFNSHTQAYATKKHCLGF	FV	ELLVLIIQNT
bovine coronavirus pol 1ab (6109)	CTKRATAY	ERTGYGWRH	SVTCYL	MLIVLIIQNG
Human corona 229E pol 1ab (5801)	CGTVATCY	MLVSNDCCFK	HALGCCYV	NYVITLIIQNG
Murine hepatitis pol 1ab (6193)	CTKRATCF	NSRTGYGWRH	SYSCYL	MLIVLIIQNG
Consensus (6319)	CTKRATCFNSRTGYG	CWKHSLGCDYLYNPLIVDI	QQNG	
Section 164				
	(6358) 6358	6370	6380	6396
avian infectious bronchitis pol 1ab (5715)	YSONLQF	DLHCNTHGHANVA	VD	MPHCLAINNATO
bovine coronavirus pol 1ab (6148)	ITSS	DLIYS	HKGAHVASSDAIMTRCLAVYDCFC	
Human corona 229E pol 1ab (5840)	YVSLST	THALCNTHRNEVA	GA	MLIVLIIQNG
Murine hepatitis pol 1ab (6232)	YVSLST	THALCNTHRNEVA	GA	MLIVLIIQNG
Consensus (6358)	YTGSLSSNHDLICSVHKG	AVASSDAIMTRCLAVYDCFC		
Section 165				
	(6397) 6397	6410	6420	6435
avian infectious bronchitis pol 1ab (5754)	QDVN	DLTYPHIAM	DEVN	SSGPHYL
bovine coronavirus pol 1ab (6187)	NNIN	NVEIT	SLLSINTSG	VLGRVMIR
Human corona 229E pol 1ab (5879)	KNVDSIT	PMIA	ENAINKGG	TV
Murine hepatitis pol 1ab (6271)	KSVN	NLEPLIS	YVSV	TSCSEL
Consensus (6397)	KNVNWNLTYP	IIANELSINTSCRL	LQRVMLRAAML	CNRY
Section 166				
	(6436) 6436	6450	6460	6474
avian infectious bronchitis pol 1ab (5793)	NVVD	ITGNEKGI	KCVRRGDV	NFR
bovine coronavirus pol 1ab (6226)	TLCY	IRDEK	---	AIACVKDFDEKFE
Human corona 229E pol 1ab (5918)	KAIH	ITGNEK	---	GIRCAVTD
Murine hepatitis pol 1ab (6310)	DVCY	ITGNEK	---	GLACVKGYDFKFE
Consensus (6436)	VCYDIGNPK	AIACVKDFDEKFEYDKNPIVKS	VTLE	
Section 167				
	(6475) 6475	6480	6490	6500
avian infectious bronchitis pol 1ab (5831)	LDYNQ	EKDKFAP	GLCMEN	NE
bovine coronavirus pol 1ab (6262)	TSFE	AHKDSEK	DOLEME	NDCEYLK
Human corona 229E pol 1ab (5955)	LDYMTAG	---	QMDGLCL	TECNVDM
Murine hepatitis pol 1ab (6346)	RYEA	KDQEL	GLCMEN	NDCEYLK
Consensus (6475)	YDYE	AHKD	FLDGLCMFWNCNV	DKYPDNAVVC
Section 168				
	(6514) 6514	6520	6530	6540
avian infectious bronchitis pol 1ab (5870)	SVFNL	PLCGNGGSLYV	NKHAFHT	TPPKEDRISERN
bovine coronavirus pol 1ab (6301)	NNL	PLCGNGGSLYV	NKHAFHT	TPPKEDRISERN
Human corona 229E pol 1ab (5992)	STLH	SECV	IGGSLYV	NNHAFHT
Murine hepatitis pol 1ab (6385)	NKL	PLCGNGGSLYV	NKHAFHT	TPPKEDRISERN
Consensus (6514)	S	LNLP	CGNGGSLYV	NKHAFHTPPFDRAAFENL

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FIGURE 4A (contd.)

Section 169																																								
	(6553)	6553	6560	6570	6580	6591																																		
avian infectious bronchitis pol 1ab (5909)		F	F	D	S	S	P	E	T	T	Q	V	D	G	V	A	Q	-	D	L	V	S	L	A	T	K	D	C	I	T	K	E	I	G	A	V	I			
bovine coronavirus pol 1ab (6340)		Y	L	S	D	T	P	C	V	Y	M	D	G	M	D	A	K	Q	V	D	Y	P	T	K	S	A	T	C	L	R	E	N	L	E	G	A	V	C		
Human corona 229E pol 1ab (6031)		Y	L	D	D	G	S	E	V	V	H	D	Q	V	N	-	-	-	-	-	Y	P	L	R	A	T	N	C	T	K	C	I	G	C	A	V	C			
Murine hepatitis pol 1ab (6424)		Y	L	S	D	T	P	C	V	Y	M	E	G	M	E	S	K	O	V	D	Y	P	T	K	S	A	T	C	L	R	E	N	L	E	G	A	V	C		
Consensus (6553)		Y	Y	S	D	T	P	C	V	Y	M	D	G	M	D	A	K	Q	V	D	Y	V	P	L	R	S	A	T	C	I	T	K	C	N	I	G	G	A	V	C
Section 170																																								
	(6592)	6592	6600	6610	6620	6630																																		
avian infectious bronchitis pol 1ab (5947)		K	K	L	A	Q	M	T	A	E	E	V	T	S	L	A	A	V	T	S	T	T	F	V	T	N	K	L	N	P	A	I	L	T	K	S	E			
bovine coronavirus pol 1ab (6379)		L	K	A	E	E	R	E	Y	L	E	S	Y	N	T	A	T	T	A	C	T	T	F	V	Y	K	T	E	D	E	F	N	L	N	T	E				
Human corona 229E pol 1ab (6066)		S	L	A	N	L	R	A	Y	W	E	I	N	I	F	T	Q	A	C	N	I	W	P	T	T	E	D	C	A	I	N	Q	I	T	E					
Murine hepatitis pol 1ab (6463)		L	K	A	E	E	R	E	Y	L	E	S	Y	N	T	A	T	T	A	C	T	T	F	V	Y	K	T	E	D	E	F	N	L	N	T	E				
Consensus (6592)		L	K	H	A	E	E	Y	R	E	Y	L	E	S	Y	N	T	A	T	T	A	G	E	T	F	W	Y	K	T	F	D	F	Y	N	L	W	N	T	F	
Section 171																																								
	(6631)	6631	6640	6650	6669																																			
avian infectious bronchitis pol 1ab (5986)		S	A	L	-	-	S	I	D	-	L	A	Y	T	M	Y	K	G	H	Y	D	A	I	A	S	E	M	T	V	I	T	G	D	A	E	M				
bovine coronavirus pol 1ab (6418)		T	K	L	-	-	S	L	E	N	I	V	Y	N	L	V	N	A	G	H	F	D	G	A	G	E	L	P	C	A	I	I	G	D	K	V	F			
Human corona 229E pol 1ab (6105)		T	K	L	-	-	S	L	E	N	I	V	Y	N	L	V	N	A	G	H	F	D	G	A	G	E	L	P	C	A	I	I	G	D	K	V	F			
Murine hepatitis pol 1ab (6502)		T	K	L	-	-	S	L	E	N	I	V	Y	N	L	V	N	A	G	H	F	D	G	A	G	E	L	P	C	A	I	I	G	D	K	V	F			
Consensus (6631)		T	K	L	-	-	Q	S	L	E	N	I	V	Y	N	L	V	N	A	G	H	F	D	G	A	G	E	L	P	C	A	I	I	G	D	K	V	F		
Section 172																																								
	(6670)	6670	6680	6690	6708																																			
avian infectious bronchitis pol 1ab (6023)		I	D	Q	G	V	E	K	A	V	F	V	T	T	L	P	T	S	V	F	F	Y	A	E	N	I	R	T	L	E	N	N	R	I	L					
bovine coronavirus pol 1ab (6455)		K	I	D	K	E	D	V	V	F	V	I	N	T	E	Y	T	N	V	V	E	L	E	A	R	P	S	I	R	H	H	E	L	K	L	F				
Human corona 229E pol 1ab (6144)		R	D	G	N	T	D	N	L	V	V	N	K	S	L	E	N	I	L	A	F	E	F	A	R	P	K	V	G	L	T	P	L	S	L	E				
Murine hepatitis pol 1ab (6539)		K	I	Q	N	E	D	V	V	V	K	N	T	P	F	F	I	N	V	V	E	L	E	A	R	P	S	I	R	P	H	E	L	K	L	F				
Consensus (6670)		K	I	Q	N	E	D	V	V	V	F	V	N	N	T	L	P	T	N	V	A	V	E	L	F	A	K	R	S	I	R	H	P	E	L	K	I	L		
Section 173																																								
	(6709)	6709	6720	6730	6747																																			
avian infectious bronchitis pol 1ab (6062)		K	G	L	G	V	D	V	T	N	G	F	T	N	L	A	N	O	T	P	L	Y	R	N	V	K	V	C	A	-	-	D	I	E	P					
bovine coronavirus pol 1ab (6494)		R	N	L	N	I	D	V	C	W	K	H	I	N	D	A	R	E	S	I	F	C	S	N	T	Y	G	V	C	M	E	E	D	L	K	E	I			
Human corona 229E pol 1ab (6183)		K	N	L	G	V	V	A	T	Y	K	F	L	N	T	E	A	R	E	L	T	S	F	T	K	S	L	G	T	-	-	D	E	A	E					
Murine hepatitis pol 1ab (6578)		R	N	L	N	I	D	V	C	W	S	H	L	A	D	A	K	D	S	V	F	C	S	S	T	Y	K	V	C	K	Y	P	D	I	O	C	L	E		
Consensus (6709)		K	N	L	N	I	D	V	T	W	K	H	V	I	W	D	Y	A	K	E	S	P	L	C	S	N	T	Y	K	V	C	A	Y	T	D	L	D	F	I	E
Section 174																																								
	(6748)	6748	6760	6770	6786																																			
avian infectious bronchitis pol 1ab (6099)		N	G	L	V	V	L	Y	D	D	R	Y	E	D	Y	O	S	T	L	A	A	D	N	A	L	V	S	T	Q	C	Y	N	R	Y	S	Y	V	E	I	
bovine coronavirus pol 1ab (6533)		K	E	N	V	L	E	D	G	R	D	N	G	A	L	E	A	K	R	S	N	I	G	Y	I	S	T	T	K	V	K	S	L	S	M	I	K	G		
Human corona 229E pol 1ab (6220)		D	V	C	T	C	Y	D	N	S	I	O	C	S	Y	E	R	E	T	L	S	T	N	A	V	L	S	A	T	A	V	T	G	G	K	S	-	-		
Murine hepatitis pol 1ab (6617)		S	L	N	V	L	E	D	G	R	D	N	G	A	L	E	A	K	K	C	R	N	G	Y	I	N	T	T	K	I	S	L	S	M	I	K	G			
Consensus (6748)		L	N	V	L	F	D	G	R	D	N	G	A	Y	E	A	F	K	K	S	N	A	V	I	S	T	T	K	V	K	S	L	S	M	I	K	G			

FIGURE 4A (contd.)

Section 175					
	(6787) 6787	6800	6810	6825	
avian infectious bronchitis pol 1ab (6138)	PSNLLVQNGMPLKDCAN-----			LYVYKRVN-	
bovine coronavirus pol 1ab (6572)	PPRAEINGVVVDKVGDTDCVFFYFAVRKEGQDVIFSOQDS				
Human corona 229E pol 1ab (6257)	LPAIKLNFQMINGNAIATVKSEDGNINKNINWFVYVRKDG				
Murine hepatitis pol 1ab (6656)	PQRADLNGVYVEKVGDSDFVFWFAVRKDGDDVIFSRGGS				
Consensus (6787)	PPRADLNGVMVDKVGDSDFVFWFAVRKDGNDVIFSR DS				
Section 176					
	(6826) 6826	6840	6850	6864	
avian infectious bronchitis pol 1ab (6163)	-----		GAFVTLPTNTN	IGSY	
bovine coronavirus pol 1ab (6611)	LRVSSNQSPQGNLGSNEPGNVGCNDALATSTIFQSRVI				
Human corona 229E pol 1ab (6286)	KPYDHYDG-----			FYVGGNTI	
Murine hepatitis pol 1ab (6695)	LEPSHYRSPQGNPGGNRVGDLSCNEALARGTIFTQSRLL				
Consensus (6826)	L VSHY SPQGN G N G L GNDALA			TIFTQSRLL	
Section 177					
	(6865) 6865	6870	6880	6890	6903
avian infectious bronchitis pol 1ab (6180)	ETTEPRSDIRHILAMSEESTVERIG-KPLGLQIIL				E
bovine coronavirus pol 1ab (6650)	SSFTCTDMEKDFLALDDDDFIQKYGLEDYAFEHIVYGN				
Human corona 229E pol 1ab (6312)	QDFLPSTMEELINMDIGVEIQKGLDFNEEFVVFED				
Murine hepatitis pol 1ab (6734)	SSFTPRSEMERKDFMDIDDDVETAKSLQYAFELVVFES				
Consensus (6865)	SSFTPRSDMEKDFLALDDDDVFIQKYGLEDYAFEHIVYGD				
Section 178					
	(6904) 6904	6910	6920	6930	6942
avian infectious bronchitis pol 1ab (6218)	VDRPQLDCEFTVITGMYLLRANKENAKSVTNSDSDVMQN				
bovine coronavirus pol 1ab (6689)	FNQKIIEFHLILGLYRQOTSNLVTOEFPVSYDSSIHSY				
Human corona 229E pol 1ab (6351)	VSKTTLFHLILSQVLSKMGILKAEEFVAASDITLKC				
Murine hepatitis pol 1ab (6773)	FNQKIIGGHLILGLARQOKSNLVTOEFPVTYDSSIHSY				
Consensus (6904)	VNQKIIGGLHLILGLYRRQQ SNLVIQEFVSYDSSIHSY				
Section 179					
	(6943) 6943	6950	6960	6970	6981
avian infectious bronchitis pol 1ab (6257)	YFVLSDNG-SYKQFIVVLELLELLELLRNILKEYGTN				
bovine coronavirus pol 1ab (6728)	FITDEKSG-GSKSVCTVIDLLLEDFVALVRSLNLCVS-				
Human corona 229E pol 1ab (6390)	CTVTYLNDPSSSTVCTYMBLLLEDFVSVLKELDITVVS-				
Murine hepatitis pol 1ab (6812)	FITDENSG-SSKSVCTVIDLLLEDFVDIVKSLNLCVS-				
Consensus (6943)	FIVDE SG SSKSVCTVIDLLLDFFVELLKSLLNLCVS				
Section 180					
	(6982) 6982	6990	7000	7010	7020
avian infectious bronchitis pol 1ab (6295)	KSKVVTMSIDYHSINFMTWFEDGSIKTCFQQLQS--ANT				
bovine coronavirus pol 1ab (6765)	--KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLQAAADWK				
Human corona 229E pol 1ab (6428)	--KQHEVILNKPWRWMLCKDNAVATFQQLQS-AEHWK				
Murine hepatitis pol 1ab (6849)	--KVVNVNIDFKDFQFMLWCNEEKVMTFPRLQAAADWK				
Consensus (6982)	KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLQAAADWK				

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FIGURE 4A (contd.)

Section 181						
	(7021)	7021	7030	7040	7059	
avian infectious bronchitis pol 1ab (6332)		CGNLEEDY	VQNCVM	PCNIPM	EVGITTLS	ILMNA
bovine coronavirus pol 1ab (6802)		PGYSLEVL	KYLNSPM	RVSLW	LEKPVTL	PTGCMNA
Human corona 229E pol 1ab (6464)		CGSLMGI	KTORMCL	PCNLY	LGAGLKL	PSGIMFN
Murine hepatitis pol 1ab (6886)		PGYVIVL	LYLESPL	LRVNLW	YCKPITI	PTGCMNA
Consensus (7021)		PGYSMPV	LYKYQNS	PLERVNL	WNYGKP	ITLPSGIMNVA
Section 182						
	(7060)	7060	7070	7080	7098	
avian infectious bronchitis pol 1ab (6371)		YTDEROYLS	KPPIC	PHMFM	MHFCAG	DRGAFGST
bovine coronavirus pol 1ab (6841)		KYQIQGL	INTITL	AVVMM	LLDCCG	SEKLVAPGSAV
Human corona 229E pol 1ab (6503)		ITTEGCF	FNSTLL	CGHNN	HWLLLG	AGNDYSAA
Murine hepatitis pol 1ab (6925)		YPTTCQGL	STTLLA	PAHNR	VLHLSA	SDKGVAZCSA
Consensus (7060)		KYTQLCQ	YLSSTT	TLCVPHN	MRVLHL	GAGSDKGVAZCSA
Section 183						
	(7099)	7099	7110	7120	7137	
avian infectious bronchitis pol 1ab (6410)		LKQWLE	PGSTLL	SNIVDY	LAHVSV	LSDNKYNTEHK
bovine coronavirus pol 1ab (6880)		LQWLE	PAGTIL	VNDNLY	PFSSV	ATYEGDCITLFPDCQ
Human corona 229E pol 1ab (6542)		LKRLE	HDALV	DNDVVDY	LA	ADFSVTGDCATVYLEDK
Murine hepatitis pol 1ab (6964)		LQWLE	PAGSTLL	SNIVDY	LAHVSV	LSDNKYNTEHK
Consensus (7099)		LKQWLE	PAGTIL	VNDNLY	PFSSV	ATYEGDCITLFPDCQ
Section 184						
	(7138)	7138	7150	7160	7176	
avian infectious bronchitis pol 1ab (6449)		FDLIIS	DMYDP	ITKNIGE	YNVSK	-----DGFETYICHFIR
bovine coronavirus pol 1ab (6919)		FDLIIS	DMYDP	ITKNIGE	YNVSK	-----DGFETYICHFIR
Human corona 229E pol 1ab (6581)		FDLIIS	DMYDP	ITKNIGE	YNVSK	-----DGFETYICHFIR
Murine hepatitis pol 1ab (7003)		FDLIIS	DMYDP	ITKNIGE	YNVSK	-----DGFETYICHFIR
Consensus (7138)		FDLIIS	DMYDP	ITKNIGE	YNVSK	-----DGFETYICHFIR
Section 185						
	(7177)	7177	7190	7200	7215	
avian infectious bronchitis pol 1ab (6488)		NNIALG	GSVAIK	ITEFSW	NAEL	SLMGKFAFWTMTFCTNV
bovine coronavirus pol 1ab (6954)		NNIALG	GSVAIK	ITEFSW	NAEL	SLMGKFAFWTMTFCTNV
Human corona 229E pol 1ab (6616)		NNIALG	GSVAIK	ITEFSW	NAEL	SLMGKFAFWTMTFCTNV
Murine hepatitis pol 1ab (7038)		NNIALG	GSVAIK	ITEFSW	NAEL	SLMGKFAFWTMTFCTNV
Consensus (7177)		NNIALG	GSVAIK	ITEFSW	NAEL	SLMGKFAFWTMTFCTNV
Section 186						
	(7216)	7216	7230	7240	7254	
avian infectious bronchitis pol 1ab (6527)		NASSSE	AFLIGIN	YLG	-----KPKVEID	GNVMHANYLFWRNS
bovine coronavirus pol 1ab (6993)		NASSSE	AFLIGIN	YLG	-----KPKVEID	GNVMHANYLFWRNS
Human corona 229E pol 1ab (6655)		NASSSE	AFLIGIN	YLG	-----KPKVEID	GNVMHANYLFWRNS
Murine hepatitis pol 1ab (7077)		NASSSE	AFLIGIN	YLG	-----KPKVEID	GNVMHANYLFWRNS
Consensus (7216)		NASSSE	AFLIGIN	YLG	-----KPKVEID	GNVMHANYLFWRNS

FIGURE 4A (contd.)

						Section 187
	(7255)	7255	7260	7270	7280	7293
avian infectious bronchitis pol 1ab (6565)		NYLOTSAY	TFVAK	DLRLKATP	VNLEKTEOKTDL	FN
bovine coronavirus pol 1ab (7030)		TVWNGGAYSIFDMAK	PLKLAGIA	TINLRADOINDM	WYS	
Human corona 229E pol 1ab (6694)		TVMSLSYNSVLLLS	FNCKHKATVVVO	KDS	DINEM	LS
Murine hepatitis pol 1ab (7114)		TVWNGGAYSIFDMAK	PLKAAGTAVVSH	KPDQINDL	LS	
Consensus (7255)		TVWNGSAYSIFDMAK	PLKLKATAVVNLK	DQINDLVLS		
						Section 188
	(7294)	7294	7300	7319		
avian infectious bronchitis pol 1ab (6604)		LIKCGLLVVDVGN	TSETSDSE	NCTM	SEQ ID NO: 9905	
bovine coronavirus pol 1ab (7069)		LIEKGGITVVD	TNKEVEVGD	SLVNI	SEQ ID NO: 9886	
Human corona 229E pol 1ab (6733)		LVRSEGLVFG	NGKCLSF	SNHLSTK	SEQ ID NO: 9914	
Murine hepatitis pol 1ab (7153)		LIEKGGITVVD	TRKEVEVGD	SLVNVK	SEQ ID NO: 9887	
Consensus (7294)		LIEKGLLVVD	TGKEVFVSD	SLVNVK		

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FIGURE 4B

		Section 1				
		(1)	1	10	20	39
human coronavirus OC43 NP	(1)	MSFTPGKQSSS-RASSGNRSGNGLK---WADQSDQVRN				
Bovine corona NP	(1)	MSFTPGKQSSS-RASFGNRSGNGLK---WADQSDQSRN				
avian infectious bronchitis virus NP	(1)	-----MASEKAAG--KSDSP--AP-				
mouse hepatitis virus NP	(1)	MSEVPGQENAGGRSSSVNRAGNGLKKTTWADQTERGPN				
Consensus	(1)	MSFTPGKQSSS RASSGNRSGNGILK WADQSDQARN				
		Section 2				
		(40)	40	50	60	78
human coronavirus OC43 NP	(36)	VQTRGRRRAQPKQTATSQQPSGGNVVPYYHWSGLTQFQK				
Bovine corona NP	(36)	VQTRGRRRAQPKQTATSQLPSGGNVVPYYHWSGLTQFQK				
avian infectious bronchitis virus NP	(16)	TIKLGPKPEVVGSSGN-----ALHQAALKAKKL				
mouse hepatitis virus NP	(40)	NQNRGRNOPIQTATTO-PNSGSVVRHYHWSGLTQFQK				
Consensus	(40)	VQTRGRRRAQPKQTATSQ PSGGNVVPYYSWFSGITQFQK				
		Section 3				
		(79)	79	90	100	117
human coronavirus OC43 NP	(75)	GKEFEFVGOPIAPGVPAATEAKLYHNRGSPHTAD				
Bovine corona NP	(75)	GKEFEFAEQVPIAPGVPAATEAKLYHNRSEHTAD				
avian infectious bronchitis virus NP	(45)	NAPAPKFEESGVVDNENLNKNSQQHNRQAL---PGK				
mouse hepatitis virus NP	(78)	GKEFOFATCOLVLANGIPASEQKLYHNRSTHTPD				
Consensus	(79)	GKEFEFAEGQGVPIAPGVPASEQQGYWYRHNRRSFKTAD				
		Section 4				
		(118)	118	130	140	156
human coronavirus OC43 NP	(114)	GNORQLLPRWYFLGTGPHAKDQYGTDLIDVYFWASNQ				
Bovine corona NP	(114)	GNORQLLPRWYFLGTGPHAKDQYTDIDVYFWASNQ				
avian infectious bronchitis virus NP	(82)	GGRAKVPDAFLTTTCEANDLNWDSQDLVFWAAG				
mouse hepatitis virus NP	(117)	QQKQLLPRWYFLGTGPHGASYGDSIEGVFWANSQ				
Consensus	(118)	GNQKQLLPRWYFYFLGTGPHAKDQYGTSIDGVFWASNQ				
		Section 5				
		(157)	157	170	180	195
human coronavirus OC43 NP	(153)	ADVNTPADIVDRDPSSDEAIPTREPPG---TVLPQGYFI				
Bovine corona NP	(153)	ADVNTPADILDSRPSSDEAIPTREPPG---TVLPQGYFI				
avian infectious bronchitis virus NP	(121)	AVKSRSNQGTPEDKFDQYLRSSDEGPDGNFRWDFIP				
mouse hepatitis virus NP	(156)	APTNRSDIVENDRPSSHEAIPTREPPG---TVLPQGFYI				
Consensus	(157)	ADVNTPADIVDRDPSSDEAIPTREPPG TVLPQGFYI				
		Section 6				
		(196)	196	210	220	234
human coronavirus OC43 NP	(189)	EGSGRSAPNSRSTSRASSRASSAGSRSRANSNGNRTPTSG				
Bovine corona NP	(189)	EGSGRSAPNSRSTSRASSRASSAGSRSRANSNGNRTPTSG				
avian infectious bronchitis virus NP	(160)	LSRAARRGRSTAASSAASSRVPSR-----EGSGRRREG				
mouse hepatitis virus NP	(192)	EGSGRSAPASRSGRSQSGPNN--RARSSSNQROPAST				
Consensus	(196)	EGSGRSAPNSRSTSRASSRASSAGSRSRANSNGNRTPTSG				

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FIGURE 4B (contd.)**Section 7**

	(235)	235	240	250	260	273
human coronavirus OC43 NP (228)		VTPDMADQIASLVLA	KLGLGKDATK	PQOV	HTAKIVRQKI	
Bovine corona NP (228)		VTPDMADQIASLVLA	KLGLGKDATK	PQOV	KQTAKEIRQKI	
avian infectious bronchitis virus NP (192)		AEDLLIARATKI	IQDQQ----	RKGTRII	QK	EEMAHRR
mouse hepatitis virus NP (229)		VKPLMAEEI	ALVLA	KLGLGKDATG	QPKQVTKOS	AKVROKI
Consensus (235)		VTPDMADQIASLVLA	KLGLGKDATK	PQOV	TKQTAKEV	RQKI

Section 8

	(274)	274	280	290	300	312
human coronavirus OC43 NP (267)		LNIPROK	SPNKQCTVQ	ICPKRGPNQ--	NGGGE	LKL
Bovine corona NP (267)		LNKPRQK	SPNKQCTVQ	CCPKRGPNQ--	NGGGE	LKL
avian infectious bronchitis virus NP (227)		FCI----	TVFPGYR	LDVHCPRTKG	KEGN	FDCKMNEE
mouse hepatitis virus NP (268)		LNKPRQK	TENKQCP	QCCFGKRGPNQ--	NGGSE	LKL
Consensus (274)		LNKPRQK	RSPNKQCTV	QCCFGKRGPNQ	NFGGGE	MLKL

Section 9

	(313)	313	320	330	340	351
human coronavirus OC43 NP (304)		GTSDPQFPILAE	IATAGAFF	FGSRLELAKVQN	----	
Bovine corona NP (304)		GTSDPQFPILAE	IATAGAFF	FGSRLELAKVQN	----	
avian infectious bronchitis virus NP (262)		GIKDGRVTAMLN	ITSPHACL	CRVTPKLQPD	GLHLRF	
mouse hepatitis virus NP (305)		GTSDPQFPILAE	IATVGF	FFFSKLEL	VKKK	----
Consensus (313)		GTSDPQFPILAE	LAPTAGAFF	FGSRLELAKVQN		

Section 10

	(352)	352	360	370	380	390
human coronavirus OC43 NP (337)		---	LSGNPDE	OKDVYELRYNGA	IRFDS	LSGFE
Bovine corona NP (337)		---	LSGNLDE	OKDVYELRYNGA	IRFDS	LSGFE
avian infectious bronchitis virus NP (301)		EFTTVVPR	DDQFIN	VKICDECMDGVG	RPKDE	VVRPK
mouse hepatitis virus NP (337)		---	SGGAE	EPTKLV	ELOYSGAV	RFDSTL
Consensus (352)			LSGN	DEPQKDVYELRYNGA	IRFDS	TLSGFETIMKV

Section 11

	(391)	391	400	410	429
human coronavirus OC43 NP (373)		LNENLNAYQQQ	DGMMNMS	PKPQRQKNGQ	----
Bovine corona NP (373)		LNENLNAYQQQ	DGMMNMS	PKPQRQKNGQ	----
avian infectious bronchitis virus NP (340)		SRPNS	----	RPATRTSSPATRQ	CKKKEKSK
mouse hepatitis virus NP (372)		LNENLNAYQK	DGADVVS	PKPQRQKNGQ	----
Consensus (391)		LNENLNAYQQQ	DGMMNMS	PKPQRQKNGQ	GENDN

Section 12

	(430)	430	440	450	468
human coronavirus OC43 NP (409)		ISVA	VPKSRVQQNKS	RELTAEDIS	LLKKMDEP
Bovine corona NP (409)		ISVA	APKSRVQQNKS	RELTAEDIS	LLKKMDEP
avian infectious bronchitis virus NP (373)		VDK	LTSDERN	---	AOIEFD
mouse hepatitis virus NP (410)		VSV	KPKSSVQR	VSRELTPETR	SLTAQILDDGVVPDGL
Consensus (430)		ISVA	LKSRVQQNKS	RELTAEDIS	LLKKMDDP

Section 13

	(469)	469	474	
human coronavirus OC43 NP (443)		EDTSEI		SEQ ID NO: 9915
Bovine corona NP (443)		EDTSEI		SEQ ID NO: 9887
avian infectious bronchitis virus NP (404)		LGENSEL		SEQ ID NO: 9906
mouse hepatitis virus NP (449)		EDDSNV		SEQ ID NO: 9898
Consensus (469)		EDTSEI		

FIGURE 4C

Section 1

	(1)	1	10	20	30	42
human coronavirus OC43 HE	(1)	----	MFLLP	RFILVSCIIGSLGTFY	P-TN	VVSHLVIGBRLLEFC
bovine coronavirus HE	(1)	----	MELLLR	EVIVSCTIGSLGTDNP	TN	VSHLVIGLMTLEFC
mouse hepatitis virus HE	(1)	MARTDAMA	PTTLLVLVSLG	YAFGFNE	LE	VSLINDLEELPES
Consensus	(1)		MFLLP	RFILVSCIIGSLGFFNPPTNVVSHLNGDWFLEFG		

Section 2

	(43)	43	50	60	70	84
human coronavirus OC43 HE	(39)	DSRS	DCNHNIVNINPH	YSSTLLN	IVVCD	ENSKACNSIFR
bovine coronavirus HE	(39)	DSRS	DCNHNIVVNTNBR	YSYDIN	PAICDELK	SKAENIFR
mouse hepatitis virus HE	(43)	DSRS	DCNHNINDSQQN	NYDDINE	ELCKGK	ATAEENLEK
Consensus	(43)	DSRS	DCNHNIVNINP	NYSYMDLNP	LCDSGKISSKAGNSIFR	

Section 3

	(85)	85	90	100	110	126
human coronavirus OC43 HE	(81)	SFHFTD	DFYNITGEG	QQIIFYEGV	NFTPYHAFKC	SGSNDIIV
bovine coronavirus HE	(81)	SFHFTD	DFYNITGEG	QQIIFYEGV	NFTPYHAFKC	SGSNDIIV
mouse hepatitis virus HE	(85)	SFHFTD	DFYNITGEG	QQIIFYEGV	NFTPYHAFKC	SGSNDIIV
Consensus	(85)	SFHFTD	DFYNITGEG	QQIIFYEGV	NFTPYHAFKC	SGSNDIIV

Section 4

	(127)	127	140	150	168
human coronavirus OC43 HE	(123)	MQNKGL	FYTQVYKNI	MAVYRSLTFV	NVPYVYNGSAQSTALCKS
bovine coronavirus HE	(123)	MQNKGL	FYTQVYKNI	MAVYRSLTFV	NVPYVYNGSAQSTALCKS
mouse hepatitis virus HE	(127)	MQNKGL	FYTQVYKNI	MAVYRSLTFV	NVPYVYNGSAQSTALCKS
Consensus	(127)	MQNKGL	FYTQVYKNI	MAVYRSLTFV	NVPYVYNGSAQSTALCKS

Section 5

	(169)	169	180	190	200	210
human coronavirus OC43 HE	(165)	GS----	LVLN	NPAYIAPOANS	GFYTKV	ADFYSGCDEYIV
bovine coronavirus HE	(165)	GS----	LVLN	NPAYIAAREAN	FGYTKV	ADFYLSGCDEYIV
mouse hepatitis virus HE	(169)	IANGVT	TLNNDTE	LGKEVSKP	ETTES	INTEQQCDEFTV
Consensus	(169)	GS	LVLN	NPAYIAKEAN	GDYYYKVEADFYLSGCDEYIV	

Section 6

	(211)	211	220	230	240	252
human coronavirus OC43 HE	(203)	PLCIF	NGKFLSNTK	YQYFSCY	LFKDTGVIY	GLNSTETITTC
bovine coronavirus HE	(203)	PLCIF	NGKFLSNTK	YQYFSCY	LFKDTGVIY	GLNSTETITTC
mouse hepatitis virus HE	(211)	PLCIF	NGKFLSNTK	YQYFSCY	LFKDTGVIY	GLNSTETITTC
Consensus	(211)	PLCIF	NGKFLSNTK	YQYFSCY	LFKDTGVIY	GLNSTETITTC

Section 7

	(253)	253	260	270	280	294
human coronavirus OC43 HE	(245)	FDLN	CHYLVLPSG	NYLAISNELLLT	VP	TKAICLNKRKDFTPV
bovine coronavirus HE	(245)	FDLN	CHYLVLPSG	NYLAISNELLLT	VP	TKAICLNKRKDFTPV
mouse hepatitis virus HE	(253)	LDLTC	IYLAITPG	YISINELLLT	VP	SKALDLRPPA
Consensus	(253)	FDLN	CHYLVLPSG	NYLAISNELLLT	VP	TKAICLNKRKDFTPV

FIGURE 4C (contd.)

Section 8

	(295)	295	300	310	320	336
human coronavirus OC43 HE (287)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
bovine coronavirus HE (287)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
mouse hepatitis virus HE (295)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
Consensus (295)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			

Section 9

	(337)	337	350	360	378
human coronavirus OC43 HE (329)		HGDAGFTSILSGLLYNSPCF	FSQQGVFRYDNVSSVWPLYPYGR		
bovine coronavirus HE (329)		HGDAGFTSILSGLLYNSPCF	FSQQGVFRYDNVSSVWPLYPYGR		
mouse hepatitis virus HE (337)		HGDAGFTSILSGLLYNSPCF	FSQQGVFRYDNVSSVWPLYPYGR		
Consensus (337)		HGDAGFTSILSGLLYNSPCF	FSQQGVFRYDNVSSVWPLYPYGR		

Section 10

	(379)	379	390	400	410	420
human coronavirus OC43 HE (371)		CPTAADIN	PDLPICVYDPLPVILLGILLGVAVIIIVVLLLY			
bovine coronavirus HE (371)		CPTAADIN	PDLPICVYDPLPVILLGILLGVAVIIIVVLLLY			
mouse hepatitis virus HE (379)		CPTAADIN	PDLPICVYDPLPVILLGILLGVAVIIIVVLLLY			
Consensus (379)		CPTAADIN	PDLPICVYDPLPVILLGILLGVAVIIIVVLLLY			

Section 11

	(421)	421	432	
human coronavirus OC43 HE (413)		FMVDNGTRLHDA		SEQ ID NO: 9916
bovine coronavirus HE (413)		FMVDNGTRLHDA		SEQ ID NO: 9888
mouse hepatitis virus HE (420)		FMVDNGTRLHDA		SEQ ID NO: 9899
Consensus (421)		FMVDNGTRLHDA		

FIGURE 4D

Section 1

	(1)	1	10	20	39
bovine coronavirus Sm	(1)	MF	MADAYFADTVWYVGQIIFIVAICLLVII	--VVVAFLA	
avian infectious bronchitis virus Sm	(1)	MN	LLNKSEENGSELTALYIIIVGFALYLLGRALQ	AVQ	
mouse hepatitis virus Sm	(1)	--MF	NLEFLDTVWYVGQIIFFAVCLMVTI	--IVVAFLA	
Consensus	(1)	M M N	FL DTVWYVGQIIFIVAICLLVII	IVVAFLA	

Section 2

	(40)	40	50	60	78
bovine coronavirus Sm	(38)	TFKLCIQ	LCGMCNTLVLS	SPSTYVFNNRG	RFYEEYN-DVK
avian infectious bronchitis virus Sm	(40)	AADA	CLFWYTWVVLPGAKGTAFVYKTYGRKLNNPELE		
mouse hepatitis virus Sm	(36)	SIKLCIQ	LCGMCNTLVLS	SPSTYLYDRSKOLYKYYNEEMR	
Consensus	(40)	S KLCIQ	LCGMCNTLVLS	PSIYLF R KQ YKFYN ELK	

Section 3

	(79)	79	90	108	
bovine coronavirus Sm	(76)	PPVLDVDDV	-----		SEQ ID NO: 9889
avian infectious bronchitis virus Sm	(79)	AVIVNEFPKNGWNNKNPANFQDAQRDKLYS			SEQ ID NO: 9907
mouse hepatitis virus Sm	(75)	LPVLDVDDI	-----		SEQ ID NO: 9900
Consensus	(79)	PILDVDDI			

	(1)	1	10	20	30	40
human coronavirus OC43 M	(1)	-MSSKTTTAPVYI	TWTADEAIKFLK	EWNFSLGII	LL	LLII
bovine coronavirus M	(1)	-MSSVTTTAPVYT	WTWTADEAIKFLK	EWNFSLGII	LL	LLII
avian infectious bronchitis virus M	(1)	-----MSNA	ANCTLDCEQSV	ELF	EYNLFITAF	LLII
mouse hepatitis virus M	(1)	MTSTTQAPQPV	QWTADEAIRFL	EWNFSLGII	LL	LLV
Consensus	(1)	MSS	TTTAPVYTWT	WTADEAIKFLK	EWNFSLGII	LLFITII

	(41)	41	50	60	70	80	
human coronavirus OC43 M	(40)	LQFG	TSRSMFV	VVIKMIILWLM	PLTIIL	TIFNV	AL
bovine coronavirus M	(40)	LQFG	TSRSMFV	VVIKMIILWLM	PLTIIL	TIFNV	AL
avian infectious bronchitis virus M	(36)	LQYGL	ATSRREI	IMVIVL	CFNEN	AVGVIS	IPF
mouse hepatitis virus M	(41)	LQFG	TSRSMFV	VVIMKMIILWLM	PLTIIV	LCIENV	AL
Consensus	(41)	LQFGYTSRSMFV	VYVIKMIILWLM	WPLTIIL	TIFNCV	YALN	

	(81)	81	90	100	110	120
human coronavirus OC43 M	(80)	NVYVGLSIVP	FTVAII	MMWIVYFVNSIR	LFIR	TGSFNS
bovine coronavirus M	(80)	NVYVGLGSIVP	FTVAII	MMWIVYFVN	ISLPIRTGSW	SFNP
avian infectious bronchitis virus M	(76)	TGGLVAAKNLEIV	ACLSEEG	WIO	IRPKGQOW	AFN
mouse hepatitis virus M	(81)	NVYVCFHSIVP	FTVAII	SIIMWIMFVN	IRPIRTGSWS	SFNP
Consensus	(81)	NVYVGLGSIVFTTIV	AIIMWIVYFVNSIR	LFIR	TGSWWSFNP	

	(121)	121	130	140	150	160
human coronavirus OC43 M (120)	ETNNLMC	IDMKGTMYVRPI	IEDYHTLT	VTTI	IRGHLYIQGI	
bovine coronavirus M (120)	ETNNLMC	IDMKGRMYVRPI	IEDYHTLT	VTTI	IRGHLYMQGI	
avian infectious bronchitis virus M (116)	ESNAVGS	ILLNGQQCNFAT	ESVPMMLS	PLIKNGVLYCEG		
mouse hepatitis virus M (121)	ETNNLMC	IDMKGTMYVRPI	IEDYHTLT	TATIRGHLYMQGV		
Consensus (121)	ETNNLMC	IDMKGTMYVRPI	IEDYHTLT	VTTI	IRGHLYMQGI	

	(161)	161	170	180	190	200	
human coronavirus OC43 M (160)	KLGT	GYSWADLI	AYMT	AKVTHL	QCT	KRGFLDRI	SDTSGF
bovine coronavirus M (160)	KLGT	GYSLSDLP	AYVT	AKVSHLLT	KRGFLDKIGD	TSGF	
avian infectious bronchitis virus M (156)	QWLAK	CEPDH	PKDIF	CPEDRNI	R-----	-----MV	
mouse hepatitis virus M (161)	KLGT	GFSLSDL	AYVT	AKVSHLCT	KRAFLDKV	DGVSGF	
Consensus (161)	KLGT	GYSLSDLP	AYVT	AKVSHLCT	KRGFLDKI	DTSGF	

	(201)	201	210	220	231	
human coronavirus OC43 M (200)	AVYVKS	GVGN	NYRLP	STQKG	SGMDT	ALLRNNI
bovine coronavirus M (200)	AVYVKS	GVGN	NYRLP	STQKG	SGMDT	ALLRNNI
avian infectious bronchitis virus M (185)	QKVTG	DQSEN	NKR	RFAT	-----	-----
mouse hepatitis virus M (201)	AVYVKS	GVGN	NYRLP	SN	KPSGMDT	ALLRI
Consensus (201)	AVYVKS	GVGN	NYRLP	STQKG	SGMDT	ALLRNNI

SEQ ID NO: 9917
SEQ ID NO: 9890
SEQ ID NO: 9908
SEQ ID NO: 9901

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FIGURE 4F

		Section 1				
		(1)	1	10	20	30
human coronavirus OC43 S	(1)	MFLILLISLPTAF	FAVIGDLKCTSDN	INDKDTGPP	PISTD	
avianinfectiousbronchitisvirusS	(1)	-----				
bovine coronavirus S	(1)	MFLILLISLPTAF	FAVIGDLKCTTVS	INDVDITGVP	PSTSTD	
mouse hepatitis virus S	(1)	MLFVFLFLF	PSCLGYIGDFRCIQLVNSNGANVSA	PSISTE		
Consensus	(1)	MFLILLISLPTAF	FAVIGDLKCTSL	IND	DTG	PSISTD
		Section 2				
		(41)	41	50	60	70
human coronavirus OC43 S	(40)	TVDVTNGLGTY	YVLD	DRVYINT	TLF	NGYYPTSGSTYRMA
avianinfectiousbronchitisvirusS	(1)	-----				
bovine coronavirus S	(40)	TVDVTNGLGTY	YVLD	DRVYINT	TLF	NGYYPTSGSTYRMA
mouse hepatitis virus S	(41)	TVEVSQGLGTY	YVLD	DRVYLNATLLLT	GYYPVDGSKFRNLA	
Consensus	(41)	TVDVTNGLGTY	YVLD	DRVYLNATLLLT	LLNGYYPTSGSTYRMA	
		Section 3				
		(81)	81	90	100	110
human coronavirus OC43 S	(80)	LKGSVLISRLW	KPFELSDEINGIFAKV	KNTKVIKDRVMY		
avianinfectiousbronchitisvirusS	(23)	SSSYVYYYQSA	FRITSGWHLOG	AYAVNISSEFN	NAGSS	
bovine coronavirus S	(80)	LKGTLLISL	TWEKEEFLSDFTN	IPAK	KNTKVEKDGVMY	
mouse hepatitis virus S	(81)	ETGTNSVSL	SWFOQYLSQFND	IFAK	ONLKTSTP	SGAT
Consensus	(81)	LKGTVLLS	SWFKPPFLSDFNNGIFAKV	KNTKVIKDAVMY		
		Section 4				
		(121)	121	130	140	150
human coronavirus OC43 S	(120)	SEFPAITIGST	FVNTSYSVVVQ	PRNTINST	QDGD	NKLOGLL
avianinfectiousbronchitisvirusS	(63)	SGCTVGI	THGGRVNVASSI	AMTAP	-----	S-----
bovine coronavirus S	(120)	SEFPAITIGST	FVNTSYSVVVQ	PRNTINST	QDGD	NKLOGLL
mouse hepatitis virus S	(121)	AYEPTTIVE	GSLEGYTSYTVVIEP	-----	YNG	-----
Consensus	(121)	SEFPAITIGST	FVNTSYSVVVQ	P	T	GNKLQGLL
		Section 5				
		(161)	161	170	180	190
human coronavirus OC43 S	(160)	EVSVCQYNMCE	YPNTICNPNG	NHRKELWH	LDTG	VVSCL
avianinfectiousbronchitisvirusS	(88)	---GMAWSS	SQFCTAHENFSD	TTVEVTHC	YKHGGC	PLTGM
bovine coronavirus S	(156)	EVSVCQYTMCE	YPNTICNPNG	NORVELWH	WDTG	VVSCL
mouse hepatitis virus S	(149)	MASVCQYTLCL	LPYTDCKPNTNG	GNKLIGFWHTD	VKPPICV	
Consensus	(161)	EISVCQYTMCE	YPNTICNPNG	N	RIELWH	DTGVVSCL
		Section 6				
		(201)	201	210	220	230
human coronavirus OC43 S	(199)	YKRNETYDVNA	DYLYFHFYQEGGTFYAY	FDTDTGVVTKFL		
avianinfectiousbronchitisvirusS	(126)	LQQNLIRVSAM	KNGQLEYNLTVSVAKYPTFR	SFQCVNNIT		
bovine coronavirus S	(195)	YKRNETYDVNA	DYLYFHFYQEGGTFYAY	FDTDTGVVTKFL		
mouse hepatitis virus S	(189)	LKRNETLVNNA	DAFYTHFYQHGGTFYAY	YADKPSATITFL		
Consensus	(201)	YKRNETYDVNA	DYLYFHFYQEGGTFYAY	FDTDTGVVTKFL		

FIGURE 4F (contd.)

Section 7						
	(241)	241	250	260	270	280
human coronavirus OC43 S	(239)	NYVLCMA	SHYYVMPITCN	----	SKLTLEYWVTPLTSRQY	
avianinfectiousbronchitisvirusS	(166)	SVYVINGDEVYTSNETIDVTSAGVYFKAGGPITYKVMREVK				
bovine coronavirus S	(235)	NYVLTGTMVLSHYVMBELTCN	----	SALTLEYWVTPLTSKQY		
mouse hepatitis virus S	(229)	SVYVINGDEVYTSNETIDVTSAGVYFKAGGPITYKVMREVK				
Consensus	(241)	SVYVLTG	ILSHYYVMPITCN	A S	LTLEYWVTPLTSRQY	
Section 8						
	(281)	281	290	300	310	320
human coronavirus OC43 S	(275)	LLAFNODGVIFNAED	CSDEMSEIKCKTQSIAPSTGVYEL			
avianinfectiousbronchitisvirusS	(206)	ALAYFVNGTAQDVIL	DCSPRGLLACQYNTGNFSDGFPP			
bovine coronavirus S	(271)	LLAFNODGVIFNAED	CSDEMSEIKCKTQSIAPSTGVYEL			
mouse hepatitis virus S	(269)	LFNENQKQVITSAYDCASSYTSEIKCKTQSMLEPSTGVYEL				
Consensus	(281)	LLAFNODGVIFNAVDC	SSFMSSEIKCKTQSIAPSTGVYEL			
Section 9						
	(321)	321	330	340	350	360
human coronavirus OC43 S	(315)	NGYTVQPIADVYRRIPNLP	CNIEAWLN	DKSVPSPLNWER		
avianinfectiousbronchitisvirusS	(246)	TNSSLVKQKFEVY	-----	ENSVNTTCTLHNFIEHN		
bovine coronavirus S	(311)	NGYTVQPIADVYRRIPNLP	CNIEAWLN	DKSVPSPLNWER		
mouse hepatitis virus S	(309)	SGYTVQPIADVYRRIPNLP	CNIEAWLN	DKSVPSPLNWER		
Consensus	(321)	NGYTVQPIADVYRRIPNLP	CNIEAWLN	DKSVPSPLNWER		
Section 10						
	(361)	361	370	380	390	400
human coronavirus OC43 S	(355)	KTFESNCNFMMS	SLMSFIQADSF	TENNIDAAKI	GMCFSSI	
avianinfectiousbronchitisvirusS	(277)	ETGALPMP	-----	SGVNIQTYQTKTAQSGYINFN	SFL	
bovine coronavirus S	(351)	KTFESNCNFMMS	SLMSFIQADSF	TENNIDAAKI	GMCFSSI	
mouse hepatitis virus S	(349)	KTFESNCNFMMS	SLMSFIQADSF	TENNIDAAKI	GMCFSSI	
Consensus	(361)	KTFESNCNFMMS	SLMSFIQADSF	TENNIDAAKI	GMCFSSI	
Section 11						
	(401)	401	410	420	430	440
human coronavirus OC43 S	(395)	TIDKFAIPNGRKVD	LQGLNLGYLQSF	NYRIDTTATSCQ	LY	
avianinfectiousbronchitisvirusS	(311)	SSFVYKESNFMYGSYHPSC	KFRLEETI	ANGLWFNSLSV	STA	
bovine coronavirus S	(391)	TIDKFAIPNGRKVD	LQGLNLGYLQSF	NYRIDTTATSCQ	LY	
mouse hepatitis virus S	(389)	SVDKFAVPRSRQV	DQGLNLSGFLQ	TANYRIDTAAT	COLH	
Consensus	(401)	SIDKFAIPNGRKVD	LQGLNLGYLQSF	NYRIDTTATSCQ	LY	
Section 12						
	(441)	441	450	460	470	480
human coronavirus OC43 S	(435)	YNLPAANVS	VSRENPSTWN	KRFGFIEDSV	FKPRPAGV	LTN
avianinfectiousbronchitisvirusS	(351)	EGP	-----	-----	LQG	----
bovine coronavirus S	(431)	YNLPAANVS	VSRENPSTWN	KRFGFIEDSV	FKPRPAGV	LTN
mouse hepatitis virus S	(429)	YTLPKNNVT	TNNHNPSSWN	RRYGFENDAGV	FGKN	-----Q
Consensus	(441)	YNLPAANVS	VSRENPSTWN	KRFGFIEDSV	FKPRPAGV	LTN

FIGURE 4F (contd.)

						Section 13
	(481)	481	490	500	510	520
human coronavirus OC43 S	(475)	HDVVYAQHCFKAPKNF	CPCKING	-SCVGS	GP-----	GKNN
avianinfectiousbronchitisvirusS	(357)	---GCKQSVFKGRATC	YAYS	YGGPS	ICKGV	YSG-----
bovine coronavirus S	(471)	HDVVYAQHCFKASTNF	CPCKLDGSLC	VGN	GE	GIDAGYKTS
mouse hepatitis virus S	(463)	HDVVYAQCCITVRSSY	PCAQPDIV	SPCTT	QTK-----	P
Consensus	(481)	HDVVYAQHCFKARSNFC	PKCL	G	LSVGS	GP K
						Section 14
	(521)	521	530	540	550	560
human coronavirus OC43 S	(509)	GIGTC	PAGTNYLTC	DN-----	LCTRP	PIT--FTGTYKCP
avianinfectiousbronchitisvirusS	(388)	-----	-----	-----	-----	-----
bovine coronavirus S	(511)	GIGTC	PAGTNYLTC	HNA	AQCDC	LCTPDELT
mouse hepatitis virus S	(497)	-----	-----	-----	-----	-----
Consensus	(521)	GIGTC	PAGTNYLTC	N	LCTPDPIT	TG YKCP
						Section 15
	(561)	561	570	580	590	600
human coronavirus OC43 S	(541)	QTKSLVGIGEHCSGLAVKSDYC	-----	GNS	QTCR	POAFLG
avianinfectiousbronchitisvirusS	(388)	-----	ELDHNF	GLIVYVTKSG	-----	-----
bovine coronavirus S	(551)	QTKYLVGIGEHCSGLAIKSDHC	-----	GNP	CTC	QPOAFLG
mouse hepatitis virus S	(497)	-KSAFVNVDHCEGIGVLEDNC	GNADPHKGC	ICANN	SEIG	
Consensus	(561)	QTKALVGIGEHCSGLAVKSDHC		GN	CTC	POAFLG
						Section 16
	(601)	601	610	620	630	640
human coronavirus OC43 S	(577)	WSADSC	LOGDKCNIFANFILH	DVNSGLT	CSTD	LKANTDI
avianinfectiousbronchitisvirusS	(407)	-----	-----	SR-	IQATE	PEPVITONHYNEL
bovine coronavirus S	(587)	WSVDS	CLOGDRCNIFANFILH	DVNSG	TUCST	DLQKSNLTI
mouse hepatitis virus S	(536)	WSHDT	CLVNDRCQIFANILLNC	INS	GTTCST	DLQLPNTTEV
Consensus	(601)	WS	DSCLOGDRCNIFANFILHD	INS	GTTCST	DLQKANTDI
						Section 17
	(641)	641	650	660	670	680
human coronavirus OC43 S	(617)	ILGVCVN	DLGITG	QIFVEVN	NATYYNSWQNL	LYDSNGN
avianinfectiousbronchitisvirusS	(427)	TLNTQ	DNITERTG	CFITN	TD	SAVS--YNYLAAGLA
bovine coronavirus S	(627)	ILGVCVN	DLGITG	QIFVEVN	NATYYNSWQNL	LYDSNGN
mouse hepatitis virus S	(576)	VTGIC	VKN	DLTG	QGV	EKKADYYNSWQTL
Consensus	(641)	ILGVCVN	YDLGITG	QIFVEVN	NATYYNSWQNL	LYDSNGN
						Section 18
	(681)	681	690	700	710	720
human coronavirus OC43 S	(657)	LYGFRDY	ITNRTFMIRSCYSGRV	SAA	FHANS	SSEPALLFRN
avianinfectiousbronchitisvirusS	(465)	ILDTSG	SIDIFVVQGEYGLNYYKVN	PCEDVN	QQFV	VSGGK
bovine coronavirus S	(667)	LYGFRDY	LTNRTFMIRSCYSGRV	SAA	FHANS	SSEPALLFRN
mouse hepatitis virus S	(616)	LNGFRDL	TNKTYTIRSCYSGRV	SAA	FHKDA	PEPALLYRN
Consensus	(681)	LYGFRDY	ITNRTFMIRSCYSGRV	SAA	FHANS	SSEPALLFRN

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FIGURE 4F (contd.)

Section 19						
	(721)	721	730	740	750	760
human coronavirus OC43 S	(697)	IKCNYVFNNISLTRQLQPINYFDSYLGCVVNAYNSTAISVQ				
avianinfectiousbronchitisvirusS	(505)	LVGILTSTRNETGSOELLENOFYIKITNGTRRRFRRSITENVA				
bovine coronavirus S	(707)	IKCNYVFNNITLSRQLQPINYFDSYLGCVVNADNSTSSVVQ				
mouse hepatitis virus S	(656)	INGSYVFSSINISREENPLNYFDSYLGCVVNADNRTDEALP				
Consensus	(721)	IKCNYVFNNISLSRQLQPINYFDSYLGCVVNADNSTSEAVQ				
Section 20						
	(761)	761	770	780	790	800
human coronavirus OC43 S	(737)	TCDLTVGSGGYCVDYSKNRRSRGAIPTGYRFTNFEFPTVNS				
avianinfectiousbronchitisvirusS	(545)	NCPYVSYGKEQIKPDG-----SIATIVPKQL				
bovine coronavirus S	(747)	TCDLTVGSGGYCVDYSTKRRSRRSITTTGYRFTNFEFPTVNS				
mouse hepatitis virus S	(696)	NQDLRMGAGLEV DYSKSRADRSVSTGYRLTTFEPTPML				
Consensus	(761)	TCDLTVGSGGYCVDYSK RRSRRSITTTGYRFTNFEFPTVNS				
Section 21						
	(801)	801	810	820	830	840
human coronavirus OC43 S	(777)	VNDSLPEVGGLYEIQIPSEFTIGNMVEEFIQTSSPKVTIDC				
avianinfectiousbronchitisvirusS	(571)	EQFVAPLFNVVTENVLTENSENLTVTDYTFRMDVQINQ				
bovine coronavirus S	(787)	VNDSLPEVGGLYEIQIPSEFTIGNMVEEFIQTSSPKVTIDC				
mouse hepatitis virus S	(736)	VNDSVQSVMDGLYEMQIPFTNTTIGHHEEFIQTRSPVTIDC				
Consensus	(801)	VNDSLPEVGGLYEIQIPSEFTIGNMVEEFIQTSSPKVTIDC				
Section 22						
	(841)	841	850	860	870	880
human coronavirus OC43 S	(817)	AAFTCCDYAACKSOLVEYGSFCDNINAILTEVNELLDTTQ				
avianinfectiousbronchitisvirusS	(611)	LQYVCGSSLDLRKLFQQSGPVCNLSVNSGOKEMEL				
bovine coronavirus S	(827)	SAFTCCDYAACKSOLVEYGSFCDNINAILTEVNELLDTTQ				
mouse hepatitis virus S	(776)	AAFTCCDNTACROOLVEYGSFCDNINAILTEVNELLDMQ				
Consensus	(841)	AAFTCCDYAACKSOLVEYGSFCDNINAILTEVNELLDTTQ				
Section 23						
	(881)	881	890	900	910	920
human coronavirus OC43 S	(857)	LQVANSLMNGVTLSTKLKDGVNENVDNINFSPLVGLGSGE				
avianinfectiousbronchitisvirusS	(651)	LNFYSSTKP-----AGFNTPVLSNVSTGEFNISILLTNPS				
bovine coronavirus S	(867)	LQVANSLMNGVTLSTKLKDGVNENVDNINFSPLVGLGSGD				
mouse hepatitis virus S	(816)	LQVASALMQGVTLSSRLPDGTSGLPDDINFSPLIGCIGST				
Consensus	(881)	LQVASSLMNGVTLSTKLKDGVNENVDNINFSPLVGLGSGS				
Section 24						
	(921)	921	930	940	950	960
human coronavirus OC43 S	(897)	CSKASS-----RSAIEDLLFDKVKLSDVGFVEAYNNCT				
avianinfectiousbronchitisvirusS	(686)	SRRKRS-----LTEDLLFTSVESVGLPTNDAYKNEF				
bovine coronavirus S	(907)	CNKVSS-----RSAIEDLLFDKVKLSDVGFVEAYNNCT				
mouse hepatitis virus S	(856)	CAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFVEAYNNCT				
Consensus	(921)	CAK SS RSAIEDLLFDKVKLSDVGFVEAYNNCT				

FIGURE 4F (contd.)

Section 25						
	(961)	961	970	980	990	1000
human coronavirus OC43 S	(930)	GCAG--	IRDLICVQSYKGIK	IRDLISENQISGYTLAATS		
avianinfectiousbronchitisvirusS	(717)	ACPLGFFKCIACAREYN	LLVLEETITAEMQALYTSSLVA			
bovine coronavirus S	(940)	GCAG--	IRDLICVQSYNGIK	IRDLISENQISGYTLAATS		
mouse hepatitis virus S	(896)	GGQE--	VRDLICVQSFNSIK	IRDLVLSQSQISGYTLTGATA		
Consensus	(961)	GCAG	IRDLICVQSYNGIKVLPPL	ISENQISGYTLAATA		
Section 26						
	(1001)	1001	1010	1020	1030	1040
human coronavirus OC43 S	(968)	ASLFPWTAAGV	YLVNVOYRIRGLGVMDVLSQNKLI			
avianinfectiousbronchitisvirusS	(757)	SMAAGGITAGATPATOL	ARINHLGILQSLLELKNQEK			
bovine coronavirus S	(978)	ASLFPWTAAGV	YLVNVOYRIRGLGVMDVLSQNKLI			
mouse hepatitis virus S	(934)	AAMFPWS	AGVYSLSVQYRIRGLGVMDVLSQNKLI			
Consensus	(1001)	ASLFPWTAAGV	YLVNVOYRIRGLGVMDVLSQNKLI			
Section 27						
	(1041)	1041	1050	1060	1070	1080
human coronavirus OC43 S	(1008)	ANAFNNALYAT	EGGFDATNSALVKIQAVVNANAEALNNLL			
avianinfectiousbronchitisvirusS	(797)	AASNNKALGHM	EGGERSSLAQQTQDFVSKQSAILTETM			
bovine coronavirus S	(1018)	ANAFNNALGATQES	DAATNSALVKIQAVVNANAEALNNLL			
mouse hepatitis virus S	(974)	ASAFNNALGATQD	GGFDATNSALGKIQSVVNANAEALNNLL			
Consensus	(1041)	ANAFNNALGAIQEG	FDATNSALVKIQAVVNANAEALNNLL			
Section 28						
	(1081)	1081	1090	1100	1110	1120
human coronavirus OC43 S	(1048)	QQLSNRFGAISASLQ	BEILSRLEDALEANAQIDRLINGRLTA			
avianinfectiousbronchitisvirusS	(837)	ASLNKNEGAL	SVTQFTYQQFD	TCNACVRLITGRSS		
bovine coronavirus S	(1058)	QQLSNRFGAISASLQ	BEILSRLEDALEANAQIDRLINGRLTA			
mouse hepatitis virus S	(1014)	NOISNRFGAISASLQ	BEILSRLEDALEANAQIDRLINGRLTA			
Consensus	(1081)	QQLSNRFGAISASLQ	BEILSRLEDALEANAQIDRLINGRLTA			
Section 29						
	(1121)	1121	1130	1140	1150	1160
human coronavirus OC43 S	(1088)	LNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSRINFC				
avianinfectiousbronchitisvirusS	(877)	LSVLASAKQAEYIRVSQORELATOR	ETATVKSIRYST			
bovine coronavirus S	(1098)	LNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSRINFC				
mouse hepatitis virus S	(1054)	LNAYLEKQLSDSTLVKFSAAQATE	VNECVKSSSRINFC			
Consensus	(1121)	LNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSRINFC				
Section 30						
	(1161)	1161	1170	1180	1190	1200
human coronavirus OC43 S	(1128)	GNGNHIISLVQNAPYGLYFIHFSYVPT	SEVTKYVTARVSPGLCI			
avianinfectiousbronchitisvirusS	(917)	GNGRAVLTIP	ENAPNGIVTHFS	TDSEFVNVT	AI	VEFCV
bovine coronavirus S	(1138)	GNGNHIISLVQNAPYGLYFIHFSYVPT	SEVTKYVTARVSPGLCI			
mouse hepatitis virus S	(1094)	GNGNHIISLVQNAPYGLYFIHFSYVPT	SEVTKYVTARVSPGLCI			
Consensus	(1161)	GNGNHIISLVQNAPYGLYFIHFSYVPT	SEVTKYVTARVSPGLCI			

FIGURE 4F (contd.)

						Section 31
	(1201)	1201	1210	1220	1230	1240
human coronavirus OC43 S (1168)	AGDRG	-----	L	PKS	YFVNVNNTWMY	IGSGYIYFEPI
avianinfectiousbronchitisvirusS (957)	KPANASQYAI	VPANGR	ITIQVNGSYI	IARDM	M	RAII
bovine coronavirus S (1178)	AGDRG	-----	L	PKS	YFVNVNNTWMF	IGSGYIYFEPI
mouse hepatitis virus S (1134)	SGDRG	-----	L	PKA	YFVODDGEKKE	IGSSYIYFEPI
Consensus (1201)	AGDRG			IAPKSGYFVNVNNTWMFT	IGSGYIYFEPI	
						Section 32
	(1241)	1241	1250	1260	1270	1280
human coronavirus OC43 S (1202)	ENNV	VVMSTCAV	NYTKAP	YVMLNTSIP	-NLPD	FKEELDQ
avianinfectiousbronchitisvirusS (997)	AGDV	TLTSEQAN	TVSVNKT	VITTFVDNDD	FDTNDEL	SKV
bovine coronavirus S (1212)	ENNV	VVMSTCAV	NYTKAP	YVMLNTSIP	-NLPD	FKEELDQ
mouse hepatitis virus S (1168)	DKNS	VIMSSCAV	NYTKAP	YVMLNTSIP	-NPPD	FKEELDQ
Consensus (1241)	ENNV	VVMSSCAV	NYTKAP	YVMLNTSIP	-NLPD	FKEELDQ
						Section 33
	(1281)	1281	1290	1300	1310	1320
human coronavirus OC43 S (1241)	FKNQTSVAP	DLSDY	--INV	TFDLQ	VMN	L
avianinfectiousbronchitisvirusS (1037)	WNDTKHEL	DFDKFN	--YT	PIELDS	IDL	OGV
bovine coronavirus S (1251)	FKNQTSVAP	DLSDY	--INV	TFDLQ	VMN	L
mouse hepatitis virus S (1207)	FKNQTSVAP	DLSDY	--INV	TFDLQ	VMN	L
Consensus (1281)	FKNQTSVAP	DLSDY	--INV	TFDLQ	VMN	L
						Section 34
	(1321)	1321	1330	1340	1350	1360
human coronavirus OC43 S (1279)	QSY	INLKD	IGTYEY	VVWVW	LLIGL	AGVAMLVLLFFI
avianinfectiousbronchitisvirusS (1075)	QSY	INLKD	IGTYEY	VVWVW	LLIGL	AGVAMLVLLFFI
bovine coronavirus S (1289)	QSY	INLKD	IGTYEY	VVWVW	LLIGL	AGVAMLVLLFFI
mouse hepatitis virus S (1247)	ESY	INLKD	IGTYEY	VVWVW	LLIGL	AGVAMLVLLFFI
Consensus (1321)	QSY	INLKD	IGTYEY	VVWVW	LLIGL	AGVAMLVLLFFI
						Section 35
	(1361)	1361	1370	1380	1390	1400
human coronavirus OC43 S (1319)	CCCTGCG	-----	TSCFK	KCGCCDD	YTG	QELVIKT
avianinfectiousbronchitisvirusS (1115)	FFM	CGCGCCG	CGFGIMPLMS	CKKSS	YTF	FDNDV
bovine coronavirus S (1329)	CCCTGCG	-----	TSCFK	KCGCCDD	YTG	QELVIKT
mouse hepatitis virus S (1287)	CCCTGCG	-----	TSCFK	KCGCCDD	YTG	QELVIKT
Consensus (1361)	CCCTGCG			TSCFKKCGCCDD	YTG	QELVIKT
						Section 36
	(1401)	1401	1408			
human coronavirus OC43 S (1350)	SHDD	----		SEQ	ID NO:	9918
avianinfectiousbronchitisvirusS (1155)	QYRPK	KSV		SEQ	ID NO:	9909
bovine coronavirus S (1360)	SHED	----		SEQ	ID NO:	9891
mouse hepatitis virus S (1318)	NIS	SHED		SEQ	ID NO:	9902
Consensus (1401)	SHDD					

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FIGURE 5

		Section 15				
	(589)	589	600	610	620	630
human coronavirus OC43 S	(565)	NS T R P Q A I L G W A S C L Q G K C N I F A N F I L H D V N S G T T C S				
bovine coronavirus S	(575)	NP C T G Q P Q A F L G W S V D S C L Q G D R C N I F A N F I L H D V A E T T C S				
mouse hepatitis virus A59 S	(524)	K G I C A N N S I G T C H I T C I V N I R Q I F A N I L N G I T S G T T C S				
Consensus	(589)	N C T C P Q A F L G W S D S C L Q G D R C N I F A N F I L H D V N S G T T C S				
		Section 16				
	(631)	631	640	650	660	672
human coronavirus OC43 S	(607)	T D L Q K A N T D I I L G V C V N Y D L Y G I T G Q G I F V E V N A T Y Y N S W Q N				
bovine coronavirus S	(617)	T D L Q K S N I D T I L G V G N E E L G L T G G I T V Y N A T E R N G W Q N				
mouse hepatitis virus A59 S	(566)	T D L Q L E N T E V V T I I K Y P I L G T T G G V I K E V K A D E N S W Q T				
Consensus	(631)	T D L Q K A N T D I I L G V C V N Y D L Y G I T G Q G I F V E V N A T Y Y N S W Q N				
		Section 17				
	(673)	673	680	690	700	714
human coronavirus OC43 S	(649)	L L Y D S N G N L Y G F R D Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P				
bovine coronavirus S	(659)	L L Y D S N G N L Y L F Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P				
mouse hepatitis virus A59 S	(608)	L L Y D V F E N I N E S O L T N K I Y T L R S C Y S G R V S A A F H A N S S E P				
Consensus	(673)	L L Y D S N G N L Y G F R D Y I T N R T F M I R S C Y S G R V S A A F H A N S S E P				
		Section 18				
	(715)	715	720	730	740	756
human coronavirus OC43 S	(691)	A L L F R N I K C N Y V F N N S L S R Q L Q P I N Y F D S Y L G C V V N A D N S T A				
bovine coronavirus S	(701)	A L L F R N I K C N Y V F N N T L S P O L Q I N A D S Y L G C V V N A D N S I S				
mouse hepatitis virus A59 S	(650)	A L L Y R F N I N G S Y V T S N I S T E E N C L N C A S Y L G C V V N A D N R T D				
Consensus	(715)	A L L F R N I K C N Y V F N N S L S R Q L Q P I N Y F D S Y L G C V V N A D N S T A				
		Section 19				
	(757)	757	770	S1 ← 780 ↓ → S2		798
human coronavirus OC43 S	(733)	I S V Q T C D L T V G S G Y C V D Y S K N R R S R S I T T G Y R F T N F E P F T V				
bovine coronavirus S	(743)	S V V Q T C D L T V G S G Y C V D Y S K N R R S R S I T T G Y R F T N F E P F T V				
mouse hepatitis virus A59 S	(692)	E A L P N G E D R M C A L C Y D Y S K S P A H R S V S T G A L T T E L L Y P				
Consensus	(757)	A V Q T C D L T V G S G Y C V D Y S K R R S R S I T T G Y R F T N F E P F T V				
		Section 20				
	(799)	799	810	820	830	840
human coronavirus OC43 S	(775)	N S V N D S L E P V G G L Y E I Q I P S E F T I G N M E E F I Q T S S P K V T I D C				
bovine coronavirus S	(785)	N S V N D S L E P V G G L Y E I Q I P S E F T I G N M E E F I Q T S S P K V T I D C				
mouse hepatitis virus A59 S	(734)	M L Y N D S V Q S M D C L Y E I Q I P S E F T I G N H E E F I Q T R S S Y T I L L				
Consensus	(799)	N S V N D S L E P V G G L Y E I Q I P S E F T I G N M E E F I Q T S S P K V T I D C				
		Section 21				
	(841)	841	850	860	870	882
human coronavirus OC43 S	(817)	A A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q				
bovine coronavirus S	(827)	S A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q				
mouse hepatitis virus A59 S	(776)	A A F V C G D N T A C R Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q				
Consensus	(841)	A A F V C G D Y A A C K S Q L V E Y G S F C D N I N A I L T E V N E L L D T T Q L Q				

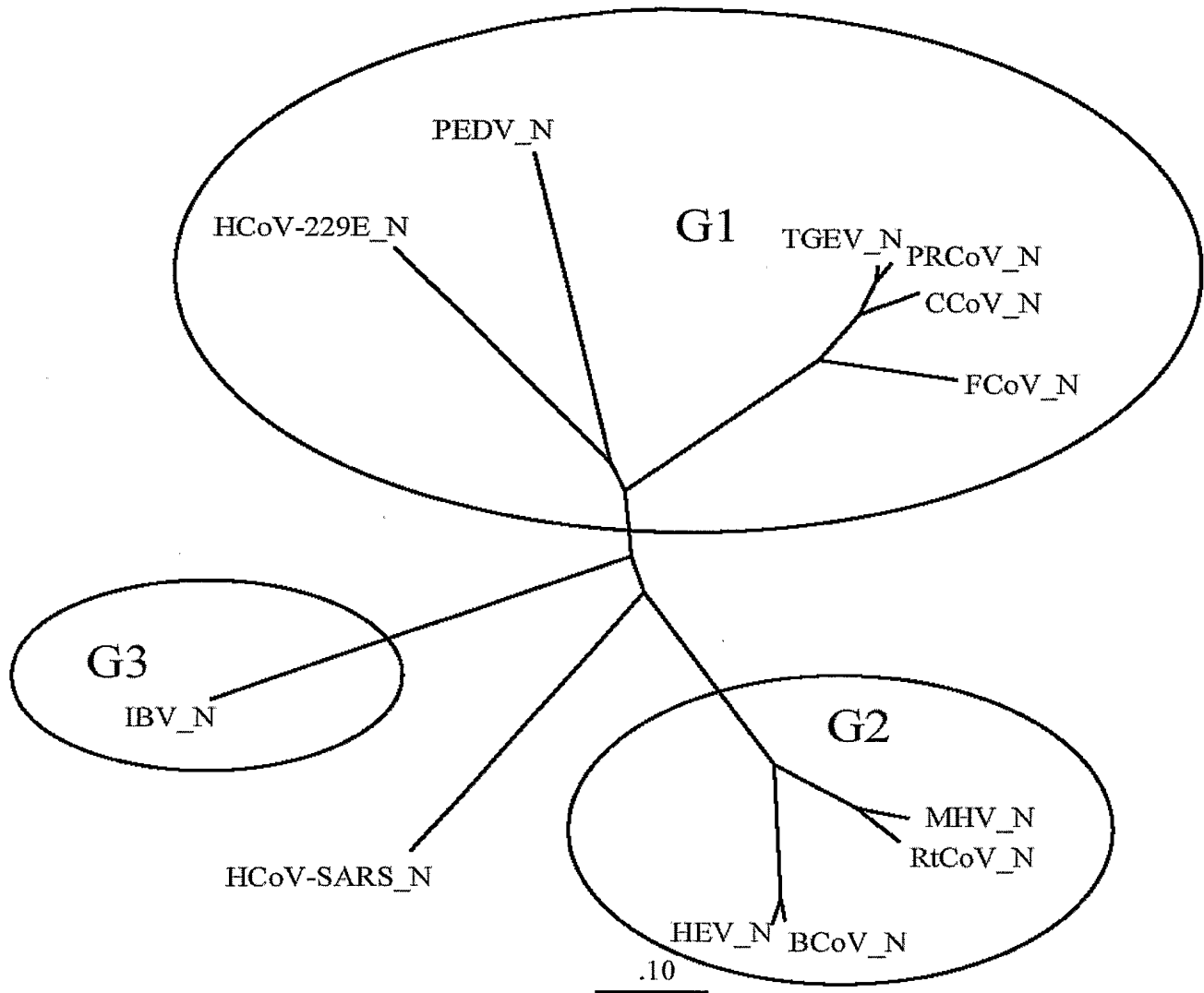
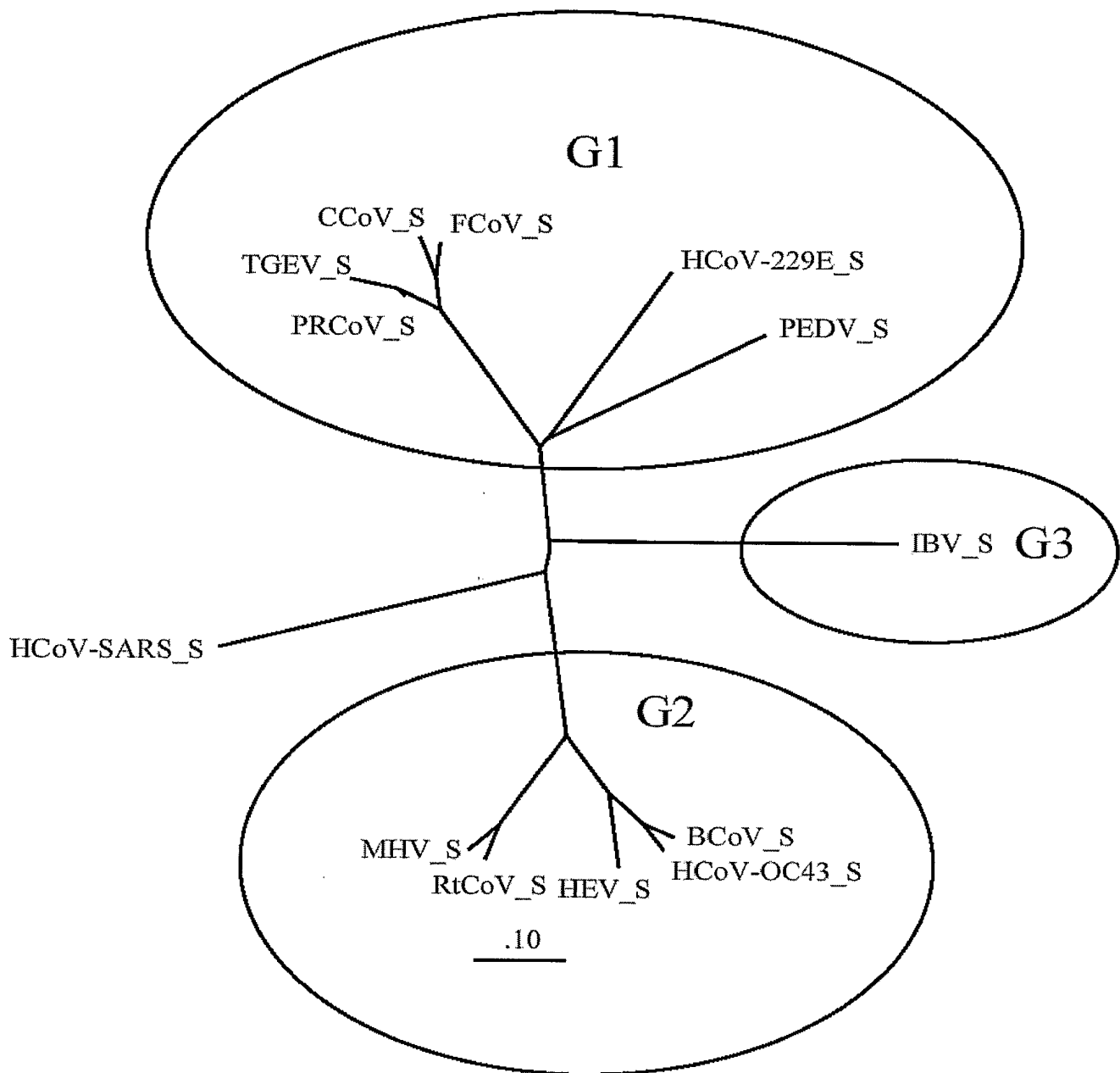
FIGURE 6**FIGURE 6A**

FIGURE 6B



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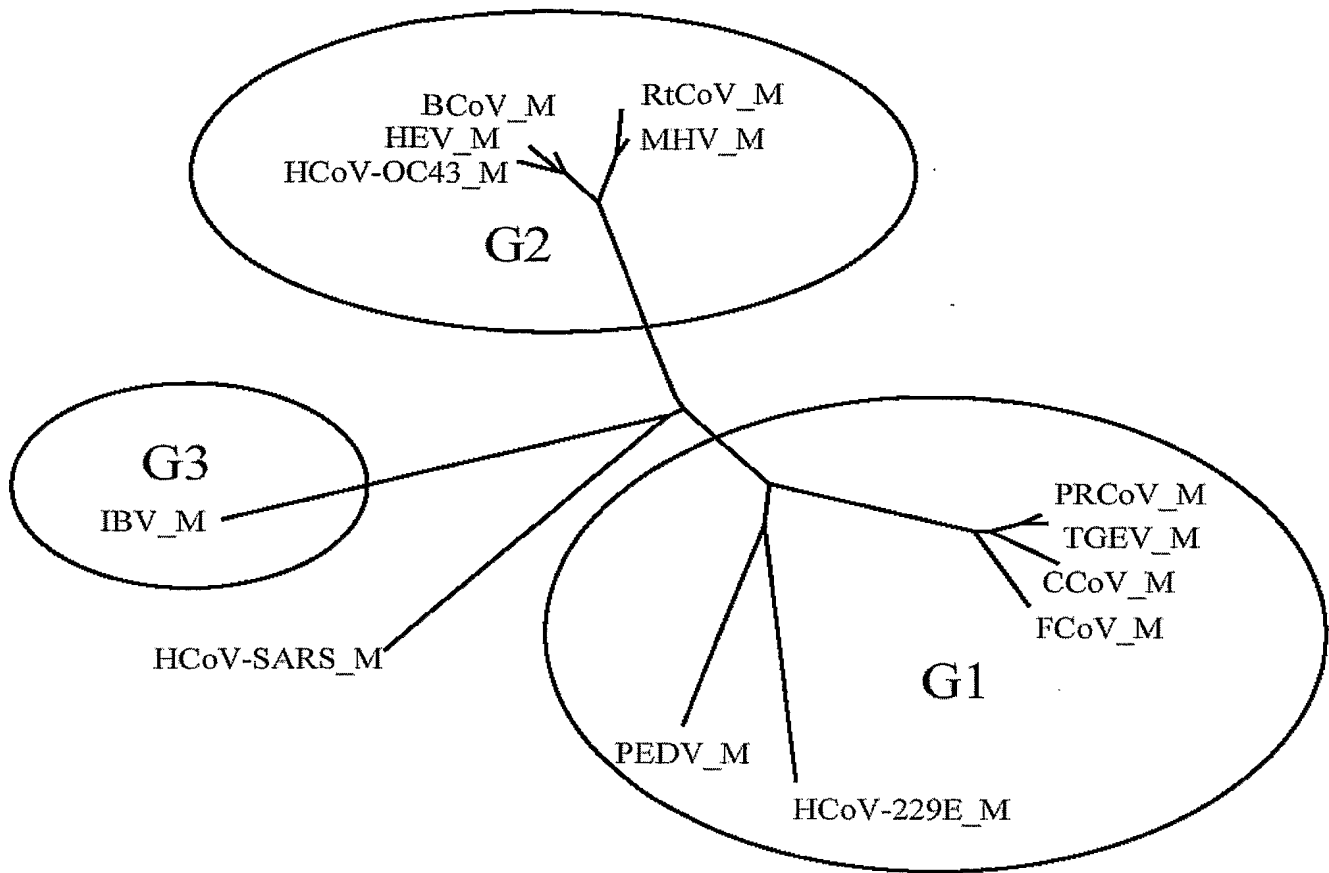
FIGURE 6C

FIGURE 7**FIGURE 7A**

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SEQ ID NO:6057 ---MKKLFVVLVVMPLIYGDNFPCSKLTNRTIGNQWNLIETFLNYSRLPPNSDVVLGD 60
SEQ ID NO:6061 ---MRSLIYFWLLLPLVPTLSLPQDVTRCQSTTNFRFFSKFN-----VQAPAVVVLGG 52
SEQ ID NO:6065 -----MFLILLISLPTAFAVIGDLKCTTVS-INDVDTGVPSIS----- 38
SEQ ID NO:6069 -----MLFVFILFLPSCGLGYIGDFRCIQLVNSNGANVSAPSIS----- 40
SEQ ID NO:6042 -----MFIFLLFLTTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRG----- 39
SEQ ID NO:6072 -----MLVTPLLLVLTLLCALCSAVLYDSSS----- 27
      :. : .

SEQ ID NO:6053 ----- 120
SEQ ID NO:6057 YFPTVQPFNCIRNDSNDLYVTLENLKALYWDYATENITWNHRQRLNVVNGYPYSITVT 120
SEQ ID NO:6061 YLPSMNSSSWYCGTGIETASGVHGIFLSYIDSGQGFEIGISQEP-----FDPSGYQLYLH 107
SEQ ID NO:6065 -----TDTVDVTNGLGTYIYVLDREVLYNTTLLNG-----YY 69
SEQ ID NO:6069 -----TETVEVSQGLGTYIYVLDREVLYNATLLLTG-----YY 71
SEQ ID NO:6042 -----VYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFG-----NP 79
SEQ ID NO:6072 -----YVYYYQSAFRPPSGWHLQG----- 46

SEQ ID NO:6053 -----IAGCQTTN-----GLNTSYSVCNG----- 31
SEQ ID NO:6057 TTRNFNSAEGAIICICKGSPPTTTTESSLTCNWGSECLRNHFKFPICPSNSEANCGNMLYG 180
SEQ ID NO:6061 KATNGNTNAIARLRICQFPDNKTLGPTVNDVTTGRNCLFNKAIPAYMRDGKDIVVGITWD 167
SEQ ID NO:6065 PTSGSTYRNMALKGTLLLSTLWFKPPFLSDFTNNGIFAKVKNKVIKDGVMYSEFPAITIG 129
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SEQ ID NO:6042 VIPFKDGIYFAATEKSNVVRGWVFGSTMNKSQSVIIINNSTNVVIRACNFELCDNPFFA 139
SEQ ID NO:6072 -----GAYAVVNISSEFNNAGSSSGCTVGIHGGRVVNASSIAMTAP----- 88

SEQ ID NO:6053 ----- 240
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SEQ ID NO:6061 -----NDRVTVFADKIIYHFYLNKNDWSRVATRCYNRRSCAMQVYVTPTYMLN----- 214
SEQ ID NO:6065 -----STFVNTSYSVVQPHTTILGNKLQGFLEISVCQYTMCEYPNT 171
SEQ ID NO:6069 -----SLFGYTSYTVVIEPN-----GVIMASVCQYTICLLPYT 165
SEQ ID NO:6042 VS-----KPMGTQHTMTIFDNAFN----- 158
SEQ ID NO:6072 -----

SEQ ID NO:6053 -----CVGYSENVFAVESGGYIPSDFAFNNWFLLTNTSSVVDGVVRSF 74
SEQ ID NO:6057 RVNNKNGTTTVSNCTDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVT 300
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SEQ ID NO:6069 DCKPNTNGNKLIGFWHTDVKPPICVLKRNFNLVNADAFYFHFYQHGGTFYAYYADKPSA 225
SEQ ID NO:6042 -CTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLYVYKGYQPIDVVRDLPSGFNTLK 217
SEQ ID NO:6072 -----SSGMAWSSSQFCTAHCNFSDTTVFVTHCYKHGG--CPLTGMLQON 131

SEQ ID NO:6053 QPLLLNCLWSVSGLRFTTGIFYFNGTGRGDCCKGFSSDVLSDVIRYNLNFEEENLRRG---T 131
SEQ ID NO:6057 QPLLVNCLWPVPSFEEAASTFCFEGAGFDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGAT 360
SEQ ID NO:6061 QPLLVNCLLAIPKIYGLGQFFSFNHTMDGVCNGAAVDRAPEALRFNINDTSVILAEG--S 332
SEQ ID NO:6065 TKFLFNVLGTVLSHYVVMLTCN----SALTLEYWVTPLTQYLLAFNQDGVIFNAVD 286
SEQ ID NO:6069 TTFLFSVYIGDILTQYYVLPFICNPTAGSTFAPRYWVTPLVKRQYLFNFNQKVITSADV 285
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SEQ ID NO:6072 LIRVSAMKNGQLFYNLTVSVAKYPTFRSFQCVNNLTSVYLNGLVYTSNETIDVTSAGVY 191

SEQ ID NO:6053 ILFKTSYG---VVVFYCTNNT-LVSGDAHIPFGTVLGNFYCFVNTTIGNETTSFAVVGAL 186
 SEQ ID NO:6057 VFSLNNTGGVTLEISCYTVSDS-SFFSYGEIPFGVTDGPRYCYVHY---NGTALKYLGTL 416
 SEQ ID NO:6061 IVLHTALG---TNLSFVCSNSSDPHLAIFAIPLGATEVPYYCFLKVDTYNSTVYKFLAVL 389
 SEQ ID NO:6065 CKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLNDKSVPS 345
 SEQ ID NO:6069 CASSYTSEIKCKTQSMPLSTGVYELSGYTVQVGVVYRRVANLPACN-IEEWLTARSVPS 344
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SEQ ID NO:6053 PKTVREFVISRTGHFYINGYRYFTLGNEAVNFNVT---TAETTDFTCTVALASYADVLV 242
 SEQ ID NO:6057 PPSVKEIAISKWGHFYINGYNFFSTFPIDCISFNLT---TGDSDFVFTIAYTSYTEALV 472
 SEQ ID NO:6061 PPTVREIVITKYGDVYVNGFGYLHLGLLDAVTINFTGHGTDDDVSQFVWTIASTNFVDALI 449
 SEQ ID NO:6065 PLNWERKTFSNCFNMSSLSMFIQAYSFTCNNIDAA---KIYGMCFSSITIDKFAIPNG 401
 SEQ ID NO:6069 PLNWERKTQNCNFNLSLLRYVQAESLFCNNIDAS---KVYGRCFGSSISVDKFAVPRS 400
SEQ ID NO:6042 VYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSAT---KLNDLCFSNVYADSFVVKGD 392
 SEQ ID NO:6072 LVKQKFIVYRENSVNTTCTLHNFIFHNETGANPNPSG--VQNIQTYQTKTAQSGYYNFNF 309

SEQ ID NO:6053 NVSQTSIANIYCNVSVINRLRCDQLSFDVPDGFYSTSP--IQSVELPVSIIVSLPVYHKHT 300
 SEQ ID NO:6057 QVENTAITKVTYCNSHVNNIKCSQITANLNGFYVSS--SEVGLVNKSVVLLPSFYTHT 530
 SEQ ID NO:6061 EVQGTISIQRILYCDPVSQKCSQVAFDLDDGFYPISSRNLLSHEQPISEFVTLPSPNDHS 509
 SEQ ID NO:6065 RKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVS--VSRFNPSTWNRFRGFTEQS 459
 SEQ ID NO:6069 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVT--INNHNPPSSWNRRYGFNDAG 458
SEQ ID NO:6042 DVRQIAPGQTGVIADYNYKLPPDDFMGCVLAWNTRNIDAT-----STGNINYKYRYLRHG 446
 SEQ ID NO:6072 SFLSSSVYKESNFMYSYHPSCFRLETINGLWFNSLS-----VSIAYGPLQGGCKQS 363

SEQ ID NO:6053 FIVLYVDFKPQ-SGGGKCFNCYPAGVNITLANFNET---KGPLCVDTSHTFTKYVAVYAN 356
 SEQ ID NO:6057 IVNITIGLGMKRSYGQPIASTLS--NITLPMQDHN---TDVYCIRSDQFS-VYVHSTCK 584
 SEQ ID NO:6061 FVNITVS-----AAFGLSSANLVASDTTINGFSS-----FCVDTRQFTITLFYNVTN 557
 SEQ ID NO:6065 VFKPQAGVFTDHDVVYAQHCFASTNFCPCKLDGSLCVGNGPGIDAGYKTSIGITCPAG 519
 SEQ ID NO:6069 VFGKN-----QHDVVYAQQCTVRSSYCPC----- 483
SEQ ID NO:6042 KLRPFER----- 453
 SEQ ID NO:6072 VFKGRAT----- 370

SEQ ID NO:6053 VGRWS-----ASINTGNCPFSFGKVN NFVKFGSVCFS LKDIPGGCAMPIVA 402
 SEQ ID NO:6057 SALWDNIFKRNCTDVLDAVIKTGTCPPSFDKLNNYLT FNKFCLSLSPVGANCKFDVAA 644
 SEQ ID NO:6061 SYGYVS-----KSQDSNCPFTLQSVNDYLSFSKFCVSTSLLAGACTIDLFG 603
 SEQ ID NO:6065 TNYLTCHNAAQCDCCLCTPDPI TSKATGPYKCPQTKYLVGIGEHCSGLAIKSDHCG----G 575
 SEQ ID NO:6069 -----AQPDIVSPCTT---QTKPKSAFVNVDHCEGLGVLEDNCGNADPH 525
SEQ ID NO:6042 -----DISNVFFSPDGKPCPTPALNCYWPLND 480
 SEQ ID NO:6072 -----CCYAYSYGGPSLCKGVYSGELDHNFECEGL 399

SEQ ID NO:6053 NWAYSKY---YTIG-----SLYVSWSDGDGITGVPQVEGVSSFMNVTLDKC 446
 SEQ ID NO:6057 -RTRTNE---QVVR-----SLYVIYEEGDNIVGVPSDNGSVHDL SVLHLDSC 687
 SEQ ID NO:6061 YPAFGSG---VKLT-----SLYFQFTKGELITGTPKPLEGITDV SFMTLDVC 647
 SEQ ID NO:6065 NPCTCQP---QAFLGWSVDSC LQGDRCNIFANFILHDVNSGTTCTSDLQKSNTDIILGVC 632
 SEQ ID NO:6069 KGCICAN---NSFIGWSDTCLVNDRCQIFANILLNGINS GTTCTSDLQLPNTDEVVTGIC 582
SEQ ID NO:6042 YGFYTTTGIGY-----QPYRVVLSFELLNAPATVCGPKLSTDLIKNQ 524
 SEQ ID NO:6072 LVYVTKS-----GGSRIQTATEPPVITQNNYNNITLNTC 433


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SEQ ID NO:6053 ---RVAGRSAIEDILFSKLVTSGLGTVDADYKCKTKGLS--IADLACAQYYNGIMVLPGV 739
SEQ ID NO:6057 ---KRKYRSAIEDLLFDKVVTSGLGTVDEDKYKCTGGYD--IADLVCAQYYNGIMVLPGV 1009
SEQ ID NO:6061 ---VVQKRSVIEDLLFNKVVTNGLGTVDEDKYKCSNGRS--VADLVCAQYYSGMVLPGV 942
SEQ ID NO:6065 ---KVSSRSAIEDLLFSKVLSDVG-FVEAYNNCTGGAE--IRDLICVQSYNGIKVLPPL 963
SEQ ID NO:6069 GPSAIRGRSAIEDLLFDKVLSDVG-FVEAYNNCTGGQE--VRDLLCVQSFNGIKVLPPI 920
SEQ ID NO:6042 -----RSFIEDLLFNKVTLDAG-FMKQYGECLGDIN--ARDLICAQKFNGLTVLPPL 846
SEQ ID NO:6072 -----RSLIEDLLFTSVESVGLP-TNDAYKNCTAGPLGFFKDLACAREYNGLLVLPPI 743

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SEQ ID NO:6053 ADAERMAMYTGSLIGGIALGGLTS----AVSIPFSLAIQARLNLYVALQTDVQLQENQKILA 795
SEQ ID NO:6057 ANADKMTMYTASLAGGITLGALGGG---AVAIPFAVAVQARLNLYVALQTDVLNKNQQILA 1066
SEQ ID NO:6061 VDAEKLHMYSASLIGGMALGGITA----AAALPFSYAVQARLNLYLALQTDVLQRNQQLLA 998
SEQ ID NO:6065 LSENQISGYTLAATSASLFPPWSA----AAGVPFYLNVQYRINGIGVTMDVLSQNQKILIA 1019
SEQ ID NO:6069 LSESQISGYTTGATAAAMFPPWSA----AAGVPFSLSVQYRINGLGVTMNVLSENQKMIA 976
SEQ ID NO:6042 LTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTONVLYENQKQIA 906
SEQ ID NO:6072 ITAEMQALYTSSLVASMAFGGITA----AGAIPFATQLQARINHLGITQSLLLKNQEKIA 799
* : . . . * : * : * : * : * : *

SEQ ID NO:6053 ASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNLSLNLTSQLRQNF 855
SEQ ID NO:6057 SAFNQAIGNITQSFGKVNDIAIHQTSRGLATVAKALAKVQDVVNIQGGQALSHLTQVLQNNF 1126
SEQ ID NO:6061 ESFNSAIGNITSFAVESVKEAISQTSKGLNTVAHALTKVQEVVNSQGSALNQLTVQLQHNF 1058
SEQ ID NO:6065 NAFNNALGAIQEGFDATN-----SALVKIQAVVNANAEALNNLLQQLSNRF 1065
SEQ ID NO:6069 SAFNNALGAIQDGFDAITN-----SALGKIQSVVNANAEALNNLLNQLSNRF 1022
SEQ ID NO:6042 NQFNKAISQIQESLTTTS-----TALGKLQDVVNQNAQALNTLVKQLSSNF 952
SEQ ID NO:6072 ASFNKAIGHMQEGFRSTS-----LALQQIQDVVSKQSAITLTETMASLNKNF 845
* * : : : * : * : * : * : *

SEQ ID NO:6053 QAISSSIQAIYDRLDTIQADQQVDRLITGRLAALNVFVSHTLTKEYTEVRASRQLAQQKVN 915
SEQ ID NO:6057 QAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKDKVN 1186
SEQ ID NO:6061 QAISSSIDDIYSRLDILSADVQVDRLITGRLSALNAFVAQTLTKYTEVQASRKLAQQKVN 1118
SEQ ID NO:6065 GAISSSLQEILSRLDALEAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVN 1125
SEQ ID NO:6069 GAISASLQEILTRLEAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIKVN 1082
SEQ ID NO:6042 GAISSVLNDILSRLDKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMS 1012
SEQ ID NO:6072 GAISSVIQEIYQQFDAIQANAQVDRLITGRLLSVLASAKQAEYIRVSQORELATQKIN 905
* * : : * : : : * : * : * : * : *

SEQ ID NO:6053 ECVKSQSKRYGFCG-NGTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAWSGLCVDG---- 970
SEQ ID NO:6057 ECVRSQSQRFGFCG-NGTHLFLSLANAAPNGMIFHTVLLPTAYETVTAWPGICASDG-DR 1244
SEQ ID NO:6061 ECVKSQSQRYGFCGGDGEHIFSLVQAAPQGLLFLHTVLVPGDFVNVLAIAGLCVNG---- 1174
SEQ ID NO:6065 ECVKSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAG---- 1180
SEQ ID NO:6069 ECVKSQTTTRINFCG-NGNHILSLVQNAPYGLYFIHFSYVPISTTANVSPGLCISG---- 1137
SEQ ID NO:6042 ECVLGQSKRVDFCG-KGYHLMSPQAAPHGVFLHVTYVPSQERNFTTAPAICHEG---- 1067
SEQ ID NO:6072 ECVKSQSIRYSFCG-NGRHVLTIPQNAPEGIVFIHFSYTPDSFVNVTAVGFCVKPANAS 964
* * : * : * : * : * : * : * : *

SEQ ID NO:6053 TNGYVLRQPNLALYK-----EGNYYRITSRIMFEPRIPTMAFVQIENCNVTFVNISRS 1024
SEQ ID NO:6057 TFGLVVKDVQLTLFRN-----LDDKFYLTPTMYQPRVATSSDFVQIEGCDVLFVNATVS 1299
SEQ ID NO:6061 EIALTLREPGLVLFTHQLQTYTATEYFVSSRRMFEPKPTVSDVQIESCVVTVYNLTSD 1234
SEQ ID NO:6065 DRGIAPKSGYFVNVNN-----TWMFTGSGYYYPEPITGNNVVMSTCAVNYTKAPDV 1232
SEQ ID NO:6069 DRGLAPKAGYFVQDDG-----EWKFTGSSYYYPEPITDKNSVIMSSCAVNYTKAPEV 1189
SEQ ID NO:6042 -KAYFPREGVVFVNGT-----SWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNT 1118
SEQ ID NO:6072 QYAIVPANGRGIFIQVN-----GSYYITARDMYMPRAITAGDVVTLTSCQANYVSVNKT 1018
* : : * : * : *

SEQ ID NO:6053 ELQTIPTV-EYIDVNKTLQELSYKL-PNYTVPDLVVEQYNQFILNLTSEISTLENKSAELN 1082
SEQ ID NO:6057 DLPSTIIP-DYIDINQTVQDILENFRPNWTVPELTFDIFNATYLNLTGEIDDLFRSEKLN 1358
SEQ ID NO:6061 QLPDVIP-DYIDVNKTLDEILASL-PNRTGPSLPLDVFNATYLNLTGEIADLEQRSESLR 1292
SEQ ID NO:6065 MLNISTP-NLPYFKEELDQWFKNQTSVAPDLSLDY--INVTFDLQDEMNN----- 1279
SEQ ID NO:6069 FLNTSIP-NPPDFKEELDQWFKNQTSIAPDLSLDFEKLNVTLTLDLTYEMN----- 1238
SEQ ID NO:6042 VYDPLQP-ELDSFKEELDKYFKNHTSPDVLGDISG-INASVVNIQKEID----- 1166
SEQ ID NO:6072 VITTFVDNDDFDFNDELKSWNDTKHELPDFDKFN--YTVPIILDIDSEID----- 1066
* : : : *

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SEQ ID NO: 6053 YTVQKLQTLIDNINSTLVDLKWLN RVET YIKWPWWVWLCISVVLIFVVSMLLLCCSTGC 1142
 SEQ ID NO: 6057 NTTVELAILIDNINNTLVNLEWLNRIET YVKWPWYVWLLIGLVVIFCIPLLFFCCSTGC 1418
 SEQ ID NO: 6061 NTTEELRSLINNINNTLV DLEWLN RVET YIKWPWWVWLIIVIVLIFVVSLLVFCCISTGC 1352
 SEQ ID NO: 6065 ----RLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWLLIGFAGVAMLVLLFFICCCTGC 1335
 SEQ ID NO: 6069 ----RIQDAIKKLNESYINLKEVGTYEMVVKWPWYVWLLIGLAGVAVCVLLFFICCCTGC 1294
SEQ ID NO: 6042 ----RLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTILLCCMTSC 1222
 SEQ ID NO: 6072 ----RIQGVIOGLNDSLIDLEKLSILKTYIKWPWYVWLAIAFATIIFILILGWVFFMTGC 1122
 .: . :*: .: :*: .: .: :*:***:*** : : : *

SEQ ID NO: 6053 CGFFSCFA-----SSIRGCCESTKLPYYD-VEKIHQ--- 1173
 SEQ ID NO: 6057 CGCIGCLG-----SCCHSICSRQFENYEPIEKVHVH--- 1450
 SEQ ID NO: 6061 CGCCGCCG-----ACFSGCCRGPRLQPYEAFEKVHVQ--- 1384
 SEQ ID NO: 6065 G--TSCFK-----KCGGCCDDYTGHQELVIKT---SHED- 1364
 SEQ ID NO: 6069 G--SCCFK-----KCGNCCDEYGGHQDSIVIHNISSHED- 1326
SEQ ID NO: 6042 CSCLKGAC-----SCG-SCCKFDEDDSEPVLKGVKLHYT- 1255
 SEQ ID NO: 6072 CGCCCGCFGIMPLMSKCGKKSSYYTTFDNDVVT EQYRPKKS V 1164

FIGURE 7B

SEQ ID NO: 6054 -----MFLKLVDHHA-LVVNVLLWCVVLLIVILLVCITIIKLIKLCFTCHMFCNRTVY 51
 SEQ ID NO: 6062 -----MLQLVNDNG-LVVNVILWLVFLVFLLIISITFVQLVNLCTCHRLCNSAVY 54
 SEQ ID NO: 6058 ---MTFPRALTVIDDNG-MVINIIFWFLIIILILLSIALLNIIKLCMVCCNLGRTVII 59
SEQ ID NO: 6045 -----MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVSLV 52
 SEQ ID NO: 6073 -----MNLLNKSLEENG-SFLTALYIIIVGFLALYLLGRALQAFVQAADACCLFWYTWWV 57
 SEQ ID NO: 6066 -----MFADAYFADTVWVVGQIIFIVAICLLVIVVVAFLATFKLCIQLCGMCNTLVL 54
 : . : . . : : . . : :

SEQ ID NO: 6054 GP----IKNVYH-IY-QSYMH-----IDPF-----PKRVIDF----- 77
 SEQ ID NO: 6062 TP----IGRLYR-VY-KSYMR-----IDPL-----PSTVIDV----- 80
 SEQ ID NO: 6058 VP----AQHAYD-AY-KNFMR-----IKAYN-----PDGALLA----- 86
SEQ ID NO: 6045 KP----TVYVYS-RV-KNLNS-----SEGV-----PDLLV----- 76
 SEQ ID NO: 6073 IPGAKGTAFVYKYTYGRKLNNPELEAVIVNEFPKNGWNNKNPANFQDAQRDKLYS 112
 SEQ ID NO: 6066 SP----SIYVFN-RG-RQFYEF-----YNDVKP-----PVLDDVDV----- 84
 * : : . *

FIGURE 7C

SEQ ID NO: 6055 -----MSNDNC-----TGDIVTHLKNWNF 19
 SEQ ID NO: 6063 -----MSNGSIP-----VDEVIEHLRNWNF 24
 SEQ ID NO: 6059 ----MKILLILACVIACACGERYCAMSDFDLSCRNSTASDCESCNGGDLIWHLANWNF 60
 SEQ ID NO: 6067 -----MSSVT-TPAPVYTWT-----ADEAIKFLKEWNF 27
 SEQ ID NO: 6070 -----MSSTQAPEPVYQWT-----ADEAVQFLKEWNF 33
SEQ ID NO: 6046 -----MADNGTIT-----VEELKQLLEQWNL 21
 SEQ ID NO: 6074 -----MPNETNCTLD-----FEQSVQLFKEYNL 28
 * . : :*: :

SEQ ID NO: 6055 GWNVILTIFIVILQFGHYKYSRLFYGLKMLVLWLLWPLVLALSIFDTWANWDSN-WAFVA 78
 SEQ ID NO: 6063 TWNIILTILLVVLQYGHYKYSVFLYGVKMAILWILWPLVLALSIFDAWASFQVN-WVFFA 83
 SEQ ID NO: 6059 SWSIILIVFITVLQYGRPQFSWFVYGIKMLIMWLLWPPVVLALTIFNAYSEYQVSRYVMFG 120
 SEQ ID NO: 6067 SLGIILLFITVILQFGYTSRSMFYVVIKMLWLMWPLTIIITIFN--CVYALN-NVYL 84
 SEQ ID NO: 6070 SLGIILLFITIILQFGYTSRSMFYVVKMILWLMWPLTIVLCIFN--CVYALN-NVYL 90
SEQ ID NO: 6046 VIGFLFLAWIMLLQFAYSNRNRFLYIILKLVFLWLLWPPVTLACFVLA--AVYRIN-WVTGG 78

SEQ ID NO:6074 FITAFLLFLTIILQYGYATRISKVIYTLKMIVLWCFWPLNIAVGVIS--CTYPPN-TGGLV 85
 :: : ** : . . . * : * : * : : : : . . .

SEQ ID NO:6055 FSFFMAVSTLVMWVMYFANSFRLFRRTFWAWNPEVNATVTTVL-GQTYQPIQQAPT 137
 SEQ ID NO:6063 FSILMACITLMLWIMYFVNSIRLWRRTHSWWSFNPETDALLTTSVM-GRQVCIPVLGAPT 142
 SEQ ID NO:6059 FSIAGAIVTFVLWIMYFVRSIQLYRRTKSWWSFNPETKAILCVSAL-GRSYVLPLEGVPT 179
 SEQ ID NO:6067 FSIVFTIVAIMWIVYFVNSIRLFI RTGSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYH 143
 SEQ ID NO:6070 FSIVFTIVSIVIWIMYFVNSIRLFI RTGSWWSFNPETNNLMCIDMK-GTVYVRPIIEDYH 149
SEQ ID NO:6046 IAIAMACIVGLMWLSYFVASFRLFARTSRMWSFNPETNILLNVPLR-GTIVTRPLMESEL 137
 SEQ ID NO:6074 AAAILTVFACLSFVGYWISIRLFKRCRSWWSFNPESNAVGSI LLTNGQQCNFAIESVPM 145
 : : : : * : * : * : * : * : * : . : *

SEQ ID NO:6055 GITVTLLSGVLYVDGHRLASGVQVHNLPEYMTVAVPSTTIIYSRVGRSVNSQNSTG--WV 195
 SEQ ID NO:6063 GVTLTLLSGTLLVEGYKVATGVQVSQLPNFVTVAKATTTIVYGRVGRSVNASSGTG--WA 200
 SEQ ID NO:6059 GVTLTLLSGNLYAEGFKIAGGMNIDNLPKYVMVALPSRTIVYTLVGKKLKASSATG--WA 237
 SEQ ID NO:6067 TLTVTIIRGHLYMQGIKLTGYSLSDLPAYVTAKVSHLLTYKRG-FLDKIGDTS--FA 200
 SEQ ID NO:6070 TLTATIIRGHLYMQGVKLTGTFSLSDLPAYVTAKVSHLCTYKRA-FLDKVDGVSG--FA 206
SEQ ID NO:6046 VIGAVIIRGHLMAGHSLGR-CDIKDLPKEITVATS-RTLSYYKLGASQRVGTDG--FA 193
 SEQ ID NO:6074 VLSPIIKNGVLYCEGQWLAK-CEPDHLPKDFVCTPDRRNIYRMVQKYTG DQSGNKKRFA 204
 : : * * * : . . . ** : * . * . . . :

SEQ ID NO:6055 FYVRVKHGDFS AVSSPMSNMTENERLLHFF 225
 SEQ ID NO:6063 FYVRSKHGDYSAVSNSAVLTDSEKVLHLV 230
 SEQ ID NO:6059 YYVKS KAGDYSTEAR-TDNLSEQEKLHLMV 266
 SEQ ID NO:6067 VYVKS KVGNYRLPSTQKGSGLDTALLRNNI 230
 SEQ ID NO:6070 VYVKS KVGNYRLPSN-KPSGADTALLR--I 233
SEQ ID NO:6046 AYNRYRIGNYKLNTHAGSNDNIALLVQ-- 221
 SEQ ID NO:6074 TFVYAKQSVDTGELESVATGSSSLYT---- 230
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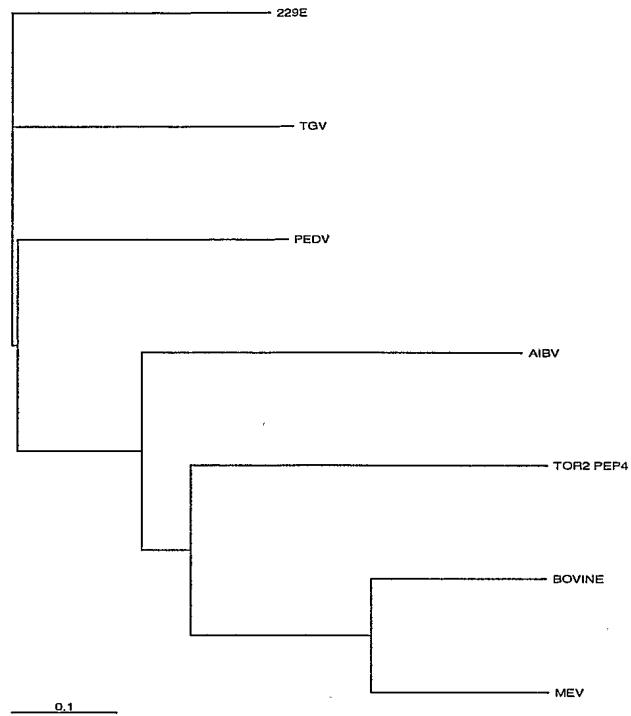
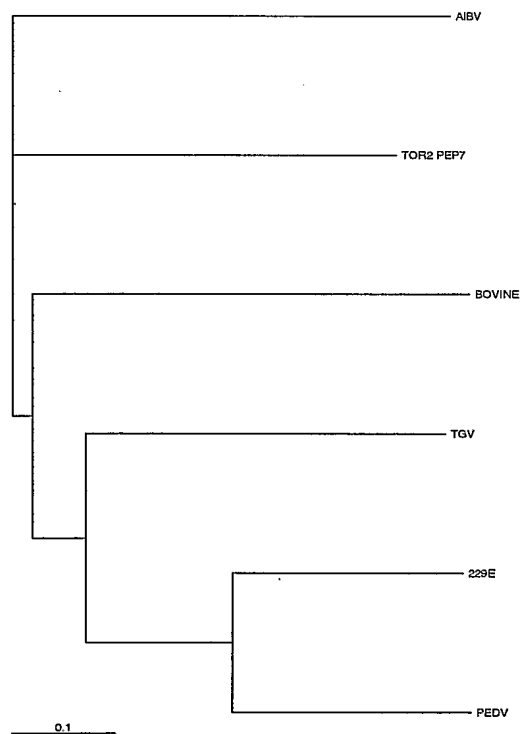
FIGURE 7D

SEQ ID NO:6056 -----MATVKWADASE-----PQRGRQG----- 18
 SEQ ID NO:6064 -----MASVSF-----QDRGRK----- 17
 SEQ ID NO:6060 -----MANQGQRVSWGDEST-----KTRGRSNSRGRKN----- 31
 SEQ ID NO:6068 MSFTPGKQSSS-RASSGNRSGNGILK---WADQSDQSRNVQTRGRR-AQPKQTATSQQPS 55
 SEQ ID NO:6071 MSFVPGQENAGGRSSSVNRAGNGILKKTWADQTERGPNNQNRGRR-NQPKQTATTQ-PN 58
SEQ ID NO:6051 -----MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPN 48
 SEQ ID NO:6075 -----MASGKAAGKTDA PAPVIKLGPKP-----PKVGSS----- 35
 . . . *

SEQ ID NO:6056 ----RIPYSLYSPLLVDSEQPW-KVIPRNLVPINKK-DKNKLIGYWN--VQKRFRTRK GK 70
 SEQ ID NO:6064 ----RVPLSLYAPLRVTNDKPLSKVLANNAVPTNKG-NKDQQIGYWN--EQIRWRMRGE 70
 SEQ ID NO:6060 ---NNIPLSFFNPITLQQGSKFWNLCP RDFVPKGIG-NRDQQIGYWN--RQTRYRMVKGQ 85
 SEQ ID NO:6068 GGNVVPYYSWFSGITQFQKGKEFEFAEQGVPIAPGVPATEAKGYWYRHNRRSFKTADGN 115
 SEQ ID NO:6071 SGSVVPYYSWFSGITQFQKGKEFQFAEQGVPIANGIPASEQKGYWYRHNRRSFKTPDGQ 118
SEQ ID NO:6051 NT-----ASWFTALTQH GK-EELRFRGQGVPIINTNSGPDDQIGYRRATRR-VRGGDGK 101
 SEQ ID NO:6075 -----GNASWFQAIKAKKLNTPPPKFEGSGVPD NENIKPSQQHGYWR--RQARFKPGKGG 88
 * : : . ** . ** : : *

SEQ ID NO:6056 RVDLSPKLHFYYLGTGPHKDAKFRERVEGVVWVAVDGAKTEPTGYGVR RNKSEPEIPHFN 130
 SEQ ID NO:6064 RIEQPSNWHFYLLGTGPHGDLRYRTRTEGVFWVAKEGAKTEPTNLGVRKASEKPIIPKFS 130
 SEQ ID NO:6060 RKELPERWFFYYLGTGPHADAKFKDKLDGVVWVAKDGAMNKPTTLGSRGANNESKALKFD 145
 SEQ ID NO:6068 QRQLLPRWYFYLLGTGPHAKDQYGTDDIDGVYVWASNQADVNTPADILDRDPSSD--EAIP 173

SEQ ID NO:6051 -PKKDKKKKTDEAQPLPQRQKKQPTVTLLPAA----- 399
SEQ ID NO:6075 NSPAPRQQRPKKEKKLKKQDDEADKALTSDEERNNAQLEFYDEPKVINWGDAALGENEL 414

FIGURE 7E**FIGURE 7F**

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FIGURE 7G

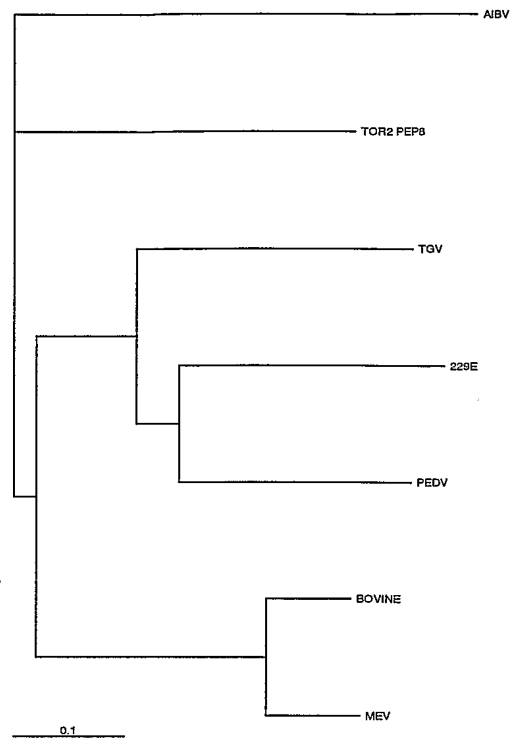


FIGURE 7H

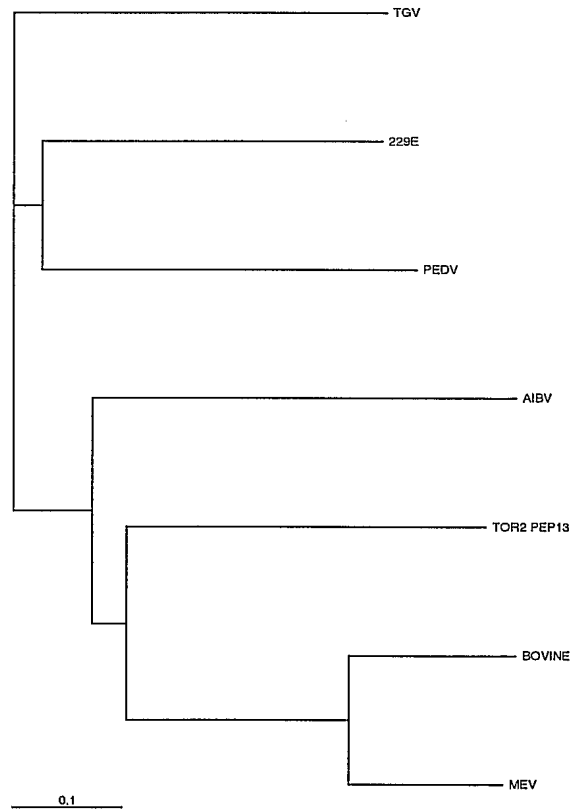


FIGURE 8

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FIGURE 9

SEQ ID NO:		
F1: AT $\frac{\text{CTT}}{\text{TGC}}$ G $\frac{\text{C}}{\text{A}}$ G $\frac{\text{GT}}{\text{CG}}$ A $\frac{\text{GGC}}{\text{TTT}}$ G $\frac{\text{G}}{\text{C}}$ GTG	(136-154 nt)	6021
F2: GTG $\frac{\text{T}}{\text{C}}$ GTG $\frac{\text{G}}{\text{C}}$ AT $\frac{\text{AG}}{\text{CC}}$ C $\frac{\text{A}}{\text{G}}$ CTTCA	(152-172 nt)	6022
F3: CTTCAC $\frac{\text{G}}{\text{T}}$ G $\frac{\text{T}}{\text{A}}$ TCT $\frac{\text{G}}{\text{C}}$ TTGT $\frac{\text{GT}}{\text{TA}}$ GA	(168-195nt)	6023
R1: AG $\frac{\text{A}}{\text{G}}$ A $\frac{\text{CCTGT}}{\text{TACAA}}$ CAC $\frac{\text{C}}{\text{G}}$ TC $\frac{\text{AGG}}{\text{CCT}}$ GG $\frac{\text{T}}{\text{C}}$ TG	(307-329nt)	6024
R2: AAA $\frac{\text{C}}{\text{T}}$ G $\frac{\text{CG}}{\text{AA}}$ TATA $\frac{\text{GC}}{\text{AA}}$ C $\frac{\text{GA}}{\text{AC}}$ C $\frac{\text{CT}}{\text{AC}}$ TATG	(265-288nt)	6025
R3: C $\frac{\text{GA}}{\text{AC}}$ C $\frac{\text{CT}}{\text{AC}}$ TATG $\frac{\text{CG}}{\text{AA}}$ A $\frac{\text{G}}{\text{A}}$ A $\frac{\text{A}}{\text{T}}$ C $\frac{\text{GTA}}{\text{TAC}}$ GCCCA	(250-274nt)	6026

FIGURE 10

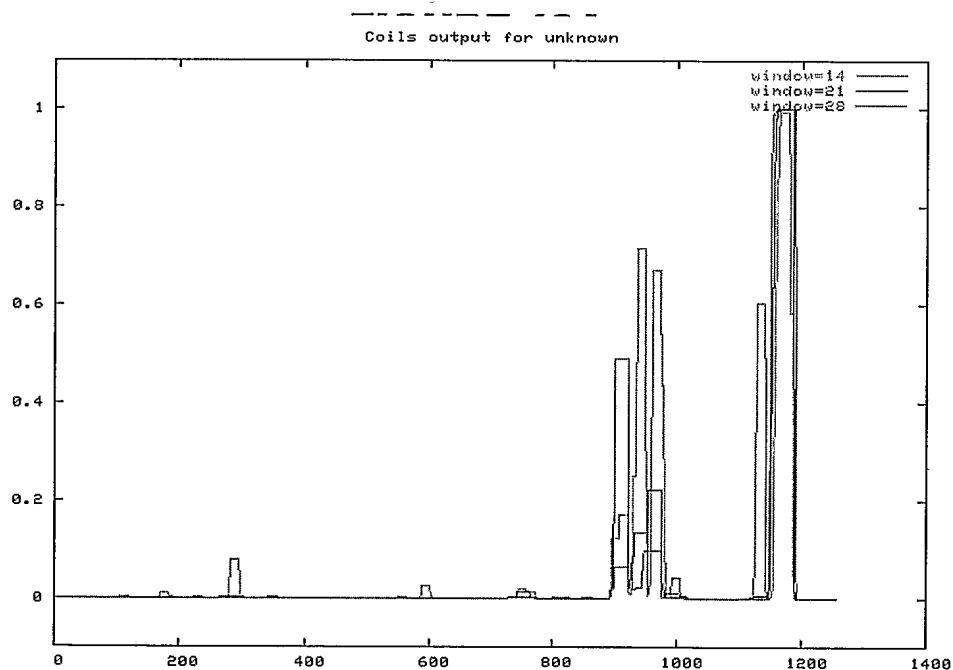
		Section 1			
		(1)	10	20	36
avian IBV 3'UTR (NC_001451) 27103-	(1)	GTAACATAATGGACCTGTTGTTTCCTGGTACATTTT			
HCoV-OC43 3'UTR partial	(1)	-----			
bovine CV 3'UTR	(1)	-----			
Consensus	(1)				
		Section 2			
		(37)	37	50	60
avian IBV 3'UTR (NC_001451) 27103-	(37)	GTTAAACACTATTTCTGTGCTTTTCCTATCAATTATT			
HCoV-OC43 3'UTR partial	(1)	-----			
bovine CV 3'UTR	(1)	-----			
Consensus	(37)				
		Section 3			
		(73)	73	80	90
avian IBV 3'UTR (NC_001451) 27103-	(73)	ACAGGCATTGATTGTGATTATGTTCAATACTTAAGC			
HCoV-OC43 3'UTR partial	(1)	-----			
bovine CV 3'UTR	(1)	-----			
Consensus	(73)				
		Section 4			
		(109)	109	120	130
avian IBV 3'UTR (NC_001451) 27103-	(109)	TTCTTTTGGTTGCTTTTGGCTTATTGTATTGTTGCT			
HCoV-OC43 3'UTR partial	(1)	-----			
bovine CV 3'UTR	(1)	-----			
Consensus	(109)				
		Section 5			
		(145)	145	150	160
avian IBV 3'UTR (NC_001451) 27103-	(145)	GTGCTTTTTTATTGTTGTGATTCTCATTAGTTTG--C			
HCoV-OC43 3'UTR partial	(1)	-----TAAGAGAATGAAC			
bovine CV 3'UTR	(1)	-----GAGAATGAAC			
Consensus	(145)	A GAGAATGAAC			
		Section 6			
		(181)	181	190	200
avian IBV 3'UTR (NC_001451) 27103-	(179)	TTTATCGTAGAAATTCAATAGTAAGAGTTAAGGAAG			
HCoV-OC43 3'UTR partial	(14)	CTTAT-GTCGGCACCTGGTGGTAACCCCTC-GCAGG			
bovine CV 3'UTR	(11)	CTTAT-GTCGGCACCTGGTGGTAACCCCTC-GCAGG			
Consensus	(181)	CTTAT GTCGGCACCTGGTGGTAACCCCTC GCAGG			
		Section 7			
		(217)	217	230	240
avian IBV 3'UTR (NC_001451) 27103-	(215)	ATAGGCATGTAGCTTGATTACCTACATGTCATATCGC			
HCoV-OC43 3'UTR partial	(48)	AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG			
bovine CV 3'UTR	(45)	AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG			
Consensus	(217)	AAAGTCGGG ATAAGGCAC TCTCTATCAG			

FIGURE 10 (contd.)

					Section 8	
	(253)	253	260	270	288	
avian IBV 3'UTR (NC_001451) 27103-	(251)	CAGGGAAATGTC	TAATCTGTC	TACTTAGTAGCCTGG		
HCoV-OC43 3'UTR partial	(76)	AATGGA	--TGTCTTGCTGCTATAATAGATAGA	---	G	
bovine CV 3'UTR	(73)	AATGGA	--TGTCTTGCTGCTATAATAGATAGA	---	G	
Consensus	(253)	AATGGA	TGTCTTGCTGCTATAATAGATAGA		G	
					Section 9	
	(289)	289	300	310	324	
avian IBV 3'UTR (NC_001451) 27103-	(287)	AAACGAACGG	TAGACCCCTAGATT	TTAATTTAGTTT		
HCoV-OC43 3'UTR partial	(107)	AAGGTTATAGCAGACTAT	-AGATT	---	AATTAGTTG	
bovine CV 3'UTR	(104)	AAGGTTATAGCAGACTAT	-AGATT	---	AATTAGTTG	
Consensus	(289)	AAGGTTATAGCAGACTAT	AGATT		AATTAGTTG	
					Section 10	
	(325)	325	330	340	350	360
avian IBV 3'UTR (NC_001451) 27103-	(323)	AAATTTT	TTAGTTT	AGTTT	AAAGTTAGT	-TTAGAGTAGG
HCoV-OC43 3'UTR partial	(139)	AAAGTTT	TGTGTGTAATGTATAGT	GTTGGAGAAAG		
bovine CV 3'UTR	(136)	AAAGTTT	TGTGTGTAATGTATAGT	GTTGGAGAAAG		
Consensus	(325)	AAAGTTT	TGTGTGTAATGTATAGT	GTTGGAGAAAG		
					Section 11	
	(361)	361	370	380	396	
avian IBV 3'UTR (NC_001451) 27103-	(358)	TATAAAGATGCCAGT	TGCCGGGGCCAC	-GCCGAGTAC		
HCoV-OC43 3'UTR partial	(175)	TG-AAAGACT	---	TGCCGGAAGTAATTGCCGACAAG		
bovine CV 3'UTR	(172)	TG-AAAGACT	---	TGCCGGAAGTAATTGCCGACAAG		
Consensus	(361)	TG AAAGACT		TGCCGGAAGTAATTGCCGACAAG		
					Section 12	
	(397)	397	410	420	432	
avian IBV 3'UTR (NC_001451) 27103-	(393)	GATCGAGGGTACAGCACTAGGACG	CCCCATTAGGGGA			
HCoV-OC43 3'UTR partial	(206)	TGCCCCAAGGGGAAGAGCCAGCAG	---	TTAAGTTA		
bovine CV 3'UTR	(203)	TGCCCCAAGGGGAAGAGCCAGCATG	---	TTAAGTTA		
Consensus	(397)	TGCCCCAAGGGGAAGAGCCAGCAG		TTAAGTTA		
					Section 13	
	(433)	433	440	450	468	
avian IBV 3'UTR (NC_001451) 27103-	(429)	AGAGCTAAATTTTAGT	--TTAAGTTAAGTTT	TAAT-T		
HCoV-OC43 3'UTR partial	(238)	CCACCCAGTAATTAGTAAATGAATGAAGTTAATTAT				
bovine CV 3'UTR	(235)	CCATCCAGTAATTAGTAAATGAATGAAGTTAATTAT				
Consensus	(433)	CCA CCAGTAATTAGTAAATGAATGAAGTTAATTAT				
					Section 14	
	(469)	469	480	490	504	
avian IBV 3'UTR (NC_001451) 27103-	(462)	GGCTAAGTATAGTTAAAATTTATAGGCTAGTATAGA				
HCoV-OC43 3'UTR partial	(274)	GGCCAATTGGAAGAATCAC	-----			
bovine CV 3'UTR	(271)	GGCCAATTGGAAGAATCAC	-----			
Consensus	(469)	GGCCAATTGGAAGAATCAC	-----			
					Section 15	
	(505)	505	513			
avian IBV 3'UTR (NC_001451) 27103-	(498)	GTTAGAGCA		SEQ ID NO: 9911		
HCoV-OC43 3'UTR partial	(293)	-----		SEQ ID NO: 9920		
bovine CV 3'UTR	(290)	-----		SEQ ID NO: 9893		
Consensus	(505)					

FIGURE 11**SEQ ID NO:**

F-1	TCTATC $\frac{GCC}{AGA}$ A $\frac{G}{T}$ GGATGTCT	(245 ~ 265 nt)	6027
F-2	TTAGTT $\frac{T}{G}$ AA $\frac{TT}{AG}$ TTT $\frac{A}{T}$ GT $\frac{T}{G}$ T $\frac{A}{G}$ GT	(318 ~ 339 nt)	6028
F-3	TAGTGTT $\frac{A}{G}$ GAG $\frac{T}{A}$ A $\frac{G}{A}$ GT $\frac{A}{G}$ TAAAGA	(346 ~ 368 nt)	6029
R-1	A $\frac{A}{C}$ TT $\frac{G}{A}$ GCCATA $\frac{A}{T}$ T $\frac{T}{A}$ AACTT	(458 ~ 476 nt)	6030
R-2	ACTAA $\frac{TTAC}{AATT}$ T $\frac{G}{A}$ G $\frac{C}{T}$ $\frac{GG}{CT}$ T $\frac{AA}{CC}$ C $\frac{T}{C}$ TAA	(426 ~ 448 nt)	6031
R-3	T $\frac{TG}{AC}$ TC $\frac{G}{C}$ GC $\frac{AA}{G}$ T $\frac{TA}{GG}$ C $\frac{TT}{CC}$ C $\frac{C}{G}$ GCA	(375 ~ 395 nt)	6032 6033

FIGURE 12

75/193

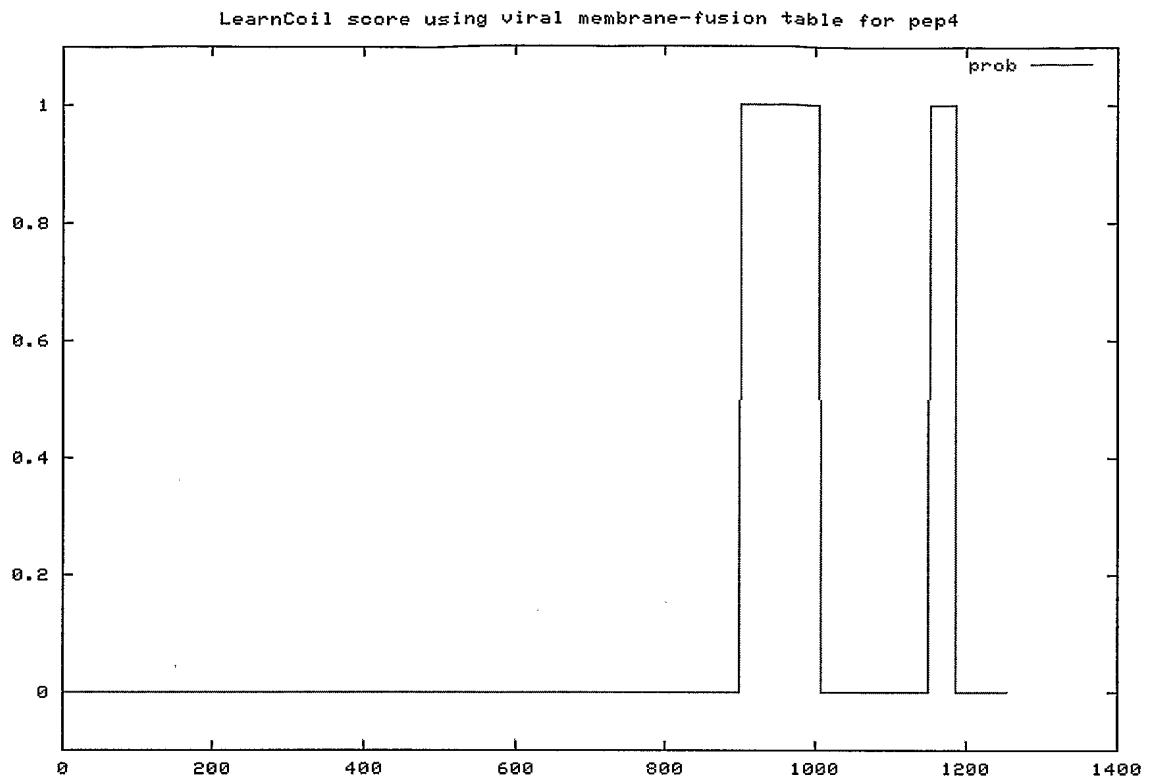
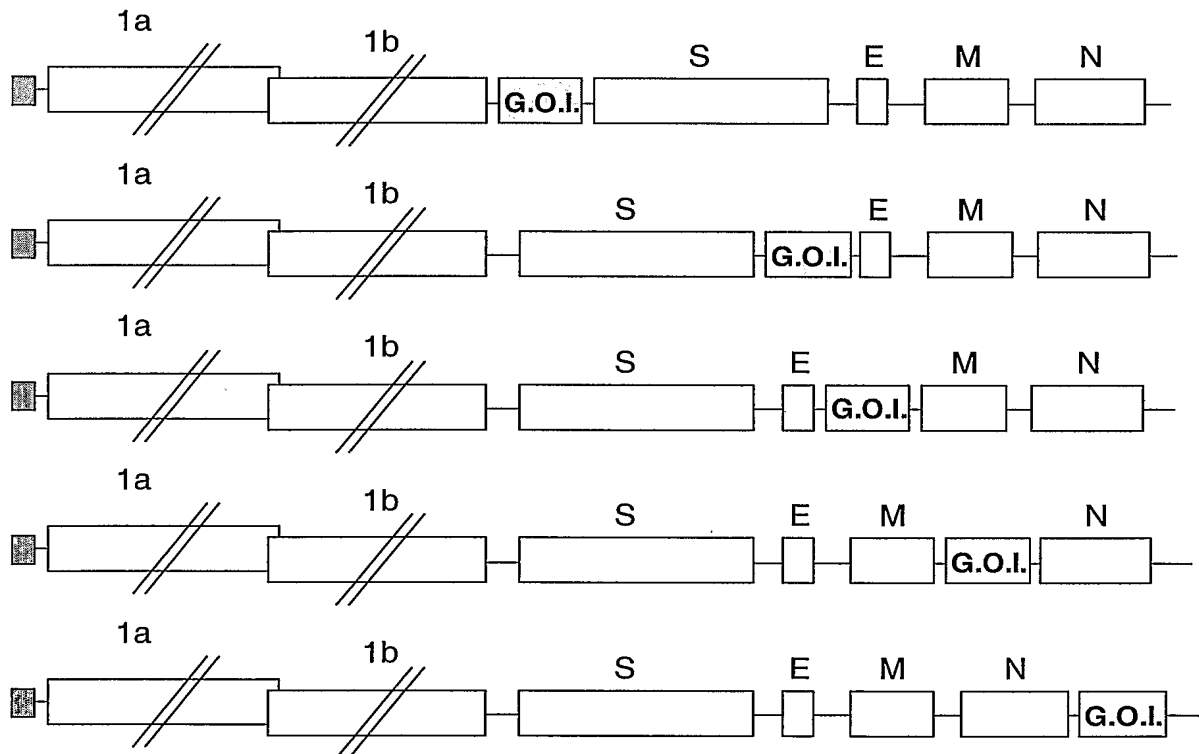
**FIGURE 13**

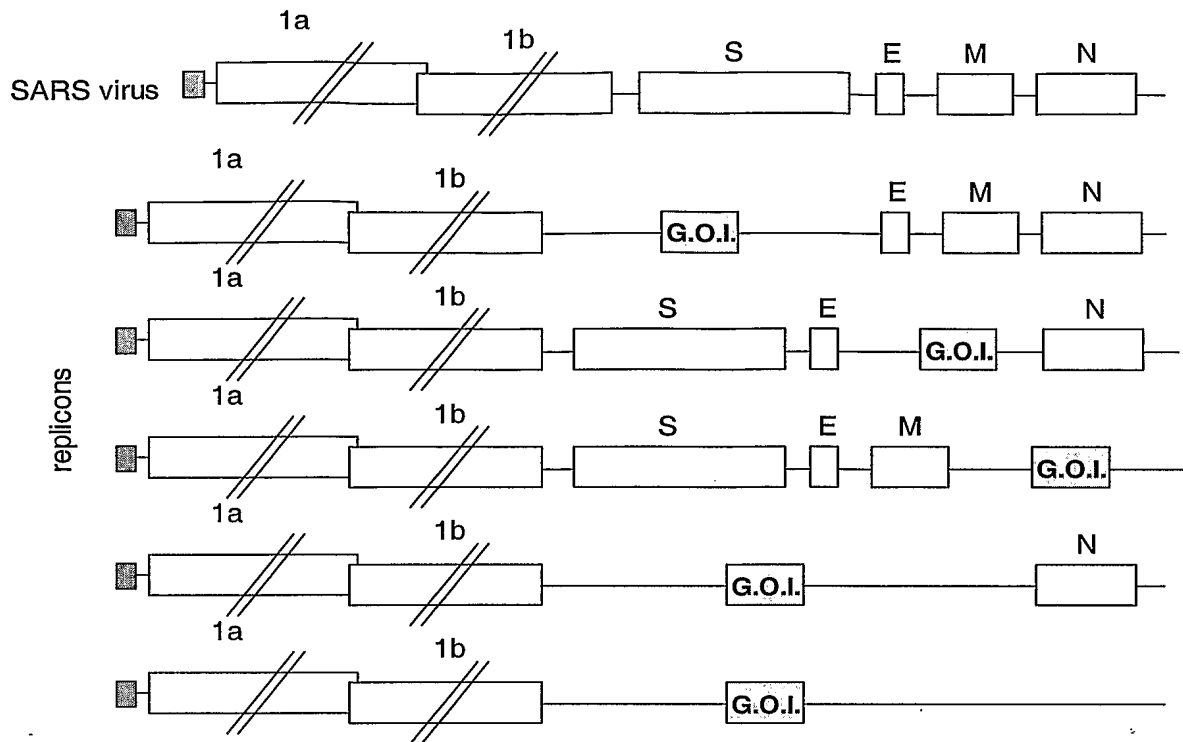
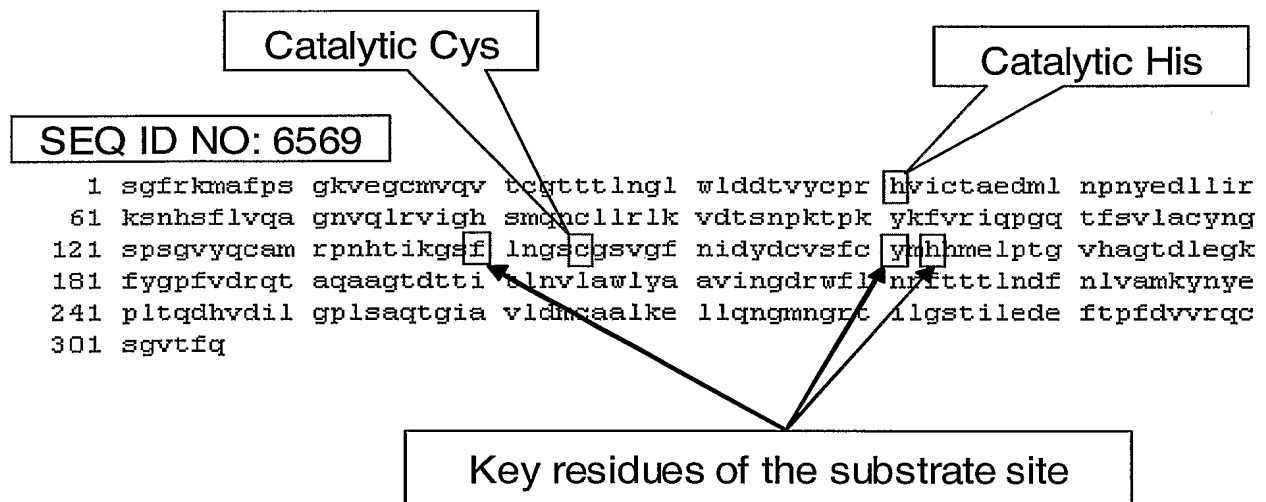
FIGURE 14**FIGURE 15**

FIGURE 16

Section 1									
	(1)	1	10	20	30	40	51		
avian IBV nsp2	(1)	SGFKALVSPSS	SAVEKCI	SVSVYRGN	NLNLGLW	LGDITTC	PRHVLIG---	KF	SG
MHV nsp2	(1)	SCIVKVMVSE	PTSKVEPC	IVSVTYGN	MTLNGLW	LDDKVYC	PRHVICSSA	DM	TD
SARS nsp2	(1)	SCFRKMAFP	SGKVEGC	IVQVTCG	TTTLNGL	WLDDITTC	PRHVIC	TAED	MLN
BCoV nsp2	(1)	SCIVKVMVSE	PTSKVEPC	IVSVTYGN	MTLNGLW	LDDKVYC	PRHVICSA	S	DMTN
Consensus	(1)	SGIVKVMVSP	SSKVEPC	IVSVTYGN	MTLNGLW	LDDTVYC	PRHVICSA	A	DMTN
Section 2									
	(52)	52	60	70	80	90	102		
avian IBV nsp2	(49)	DQNDCLNL	ANNHFE	VTTHQHG	VTLNV	VSRRLEG	AMLLQTA	MANA	ETPKY
MHV nsp2	(52)	PDYPNLL	CRVTSS	DFCUM	SGR-	SLTVMS	YQMGG	COLV	LTVTLQNP
SARS nsp2	(52)	ENYEDLL	IRKSNH	SFLVO	AGN-VOL	RVIG	SMQNC	LLBLK	VDTSNPTPKY
BCoV nsp2	(52)	PDYTNLL	CRVTSS	DFTVF	DR-	SLTVMS	YQMGG	COLV	LTVTLQNSRTPKY
Consensus	(52)	PDY NLL	CRVTSS	DF VLSGR	VSLTVMS	YQMGG	CLLV	LTVTLQ	NPKTPKY
Section 3									
	(103)	103	110	120	130	140	153		
avian IBV nsp2	(100)	KFIKANCC	DSFTT	ACATGG	TVVGL	PPVTMR	SNGTIRAS	LAGA	CGSVG
MHV nsp2	(102)	SFGVVK	PGETFT	VLAA	YNGRP	QGAHV	TMRSSHT	IKGS	FLCGS
SARS nsp2	(102)	KFVRIO	FQGF	VLAC	YNGP	SGVYQC	AMPNHT	IKGS	FLNGS
BCoV nsp2	(102)	TFGVVK	PGETFT	VLAA	YNGK	PQGAHV	TMRSSHT	IKGS	FLCGS
Consensus	(103)	KFGVVK	PGETFT	VLAA	YNGSP	QGAHV	TMRSSHT	IKGS	FLCGS
Section 4									
	(154)	154	160	170	180	190	204		
avian IBV nsp2	(151)	KGVVNFF	MHLEL	PNLHT	GTDLMO	FTYGG	VYLEE	VAQR	VPPDN
MHV nsp2	(153)	TGDSV	FVVM	MLEL	TGCH	TGTD	FSCH	PFYCP	YRDAQV
SARS nsp2	(153)	YDCVS	FCVM	MLEL	PTGV	HAGTD	DECK	FTGFP	VDRQTA
BCoV nsp2	(153)	MGDCV	KFVVM	MLEL	TGCH	TGTD	FNCH	PFYGP	YKDAQV
Consensus	(154)	DGDCV	KFVVM	MLEL	TGCH	TGTD	L	GDFYGP	YVDAQV
Section 5									
	(205)	205	210	220	230	240	255		
avian IBV nsp2	(202)	VVAWLYAA	AIISV	KESSF	SLPKW	LESTTV	SVDDY	MKWAG	DNGFPP
MHV nsp2	(204)	VVAWLYAA	IFNRCN	-----	WFOQSD	CSLE	EDFN	VWAM	NGESS
SARS nsp2	(204)	VVAWLYAA	YINGDR	-----	WFLNR	FTT	TLNDF	HLVAM	KYHPE
BCoV nsp2	(204)	VVAWLYAA	ITLNNCN	-----	WFOQSD	KCS	WEDFN	VWAL	SNGFS
Consensus	(205)	VVAWLYAA	AIIN CN		WFLQSD	TCS	LEDFN	VWAM	SNGFS
Section 6									
	(256)	256	270	280	290	306			
avian IBV nsp2	(251)	ATKL	SAITG	VDVCK	LLRTIM	VKNS-Q	GGDP	ILGQ	YNF
MHV nsp2	(247)	VIDALA	SMTGV	VEQV	LAAIK	RLHS-G	FQGR	QILG	SCVLE
SARS nsp2	(249)	ILGFL	SAQTC	IAVL	DMCAAL	KELLQ	NGM	RTIL	GSTILE
BCoV nsp2	(247)	VIDALA	SMTGV	SLETL	LAAIK	RLKN-G	FQGR	QILG	SCSFE
Consensus	(256)	VIDALA	AAMTGV	SVE	LLAAIK	RL S	GFGGR	QILG	SCILE
Section 7									
	(307)	307	313						
avian IBV nsp2	(301)	IGGVRLQ		SEQ ID NO: 6570					
MHV nsp2	(297)	LAGVKLQ		SEQ ID NO: 6571					
SARS nsp2	(300)	CSGVTFQ		SEQ ID NO: 6569					
BCoV nsp2	(297)	LAGVKLQ		SEQ ID NO: 6572					
Consensus	(307)	LAGVKLQ		SEQ ID NO: 6573					

FIGURE 17

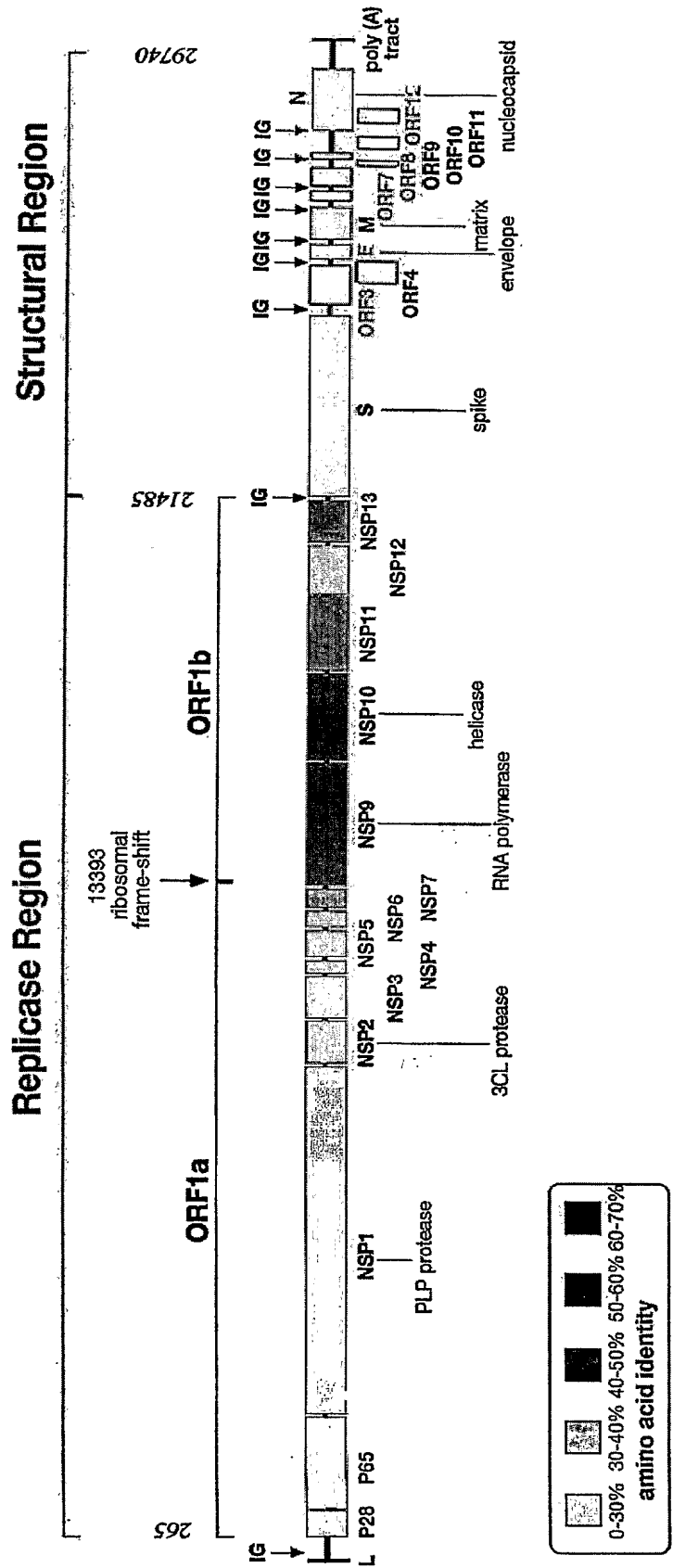


FIGURE 18

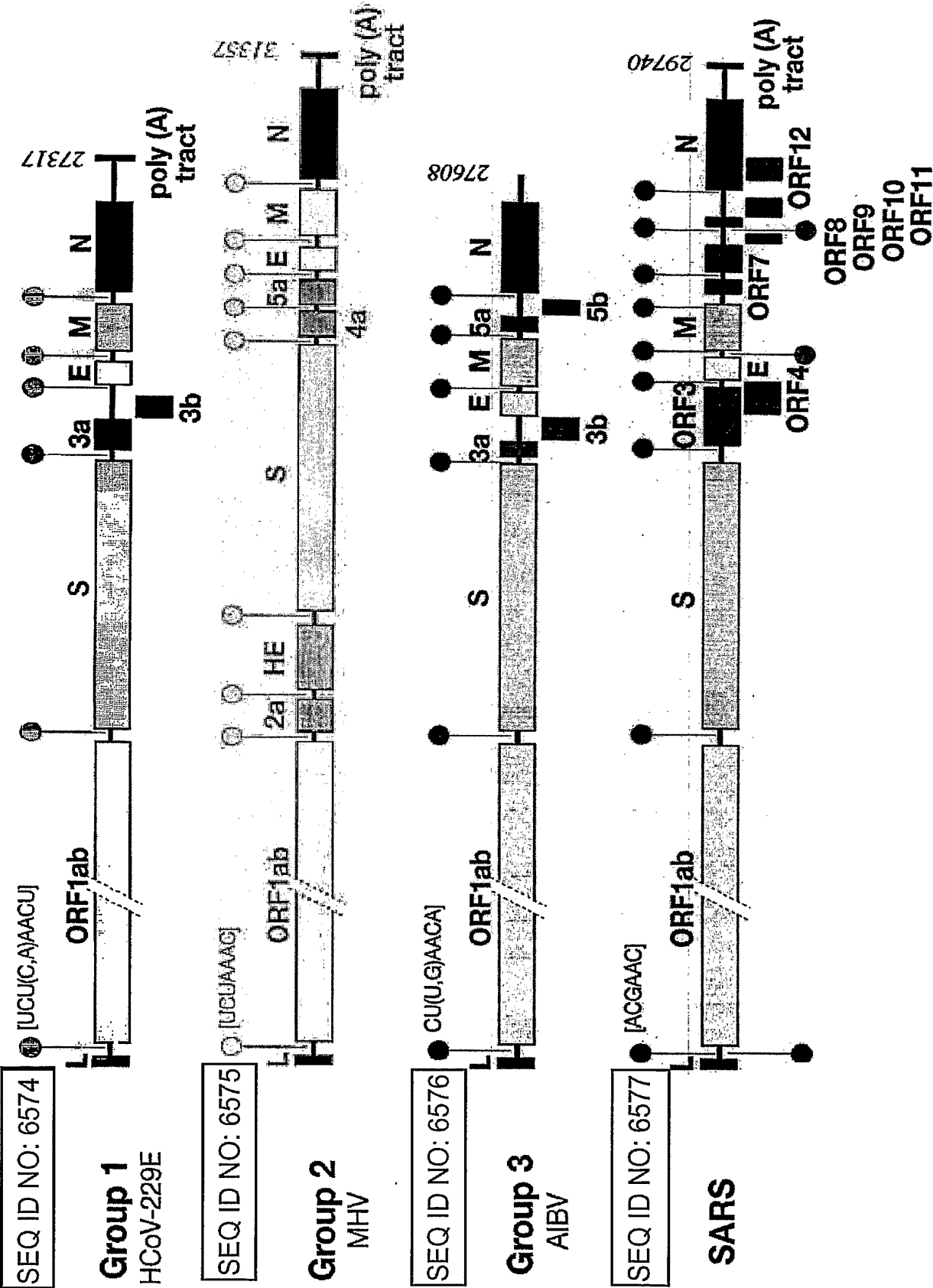


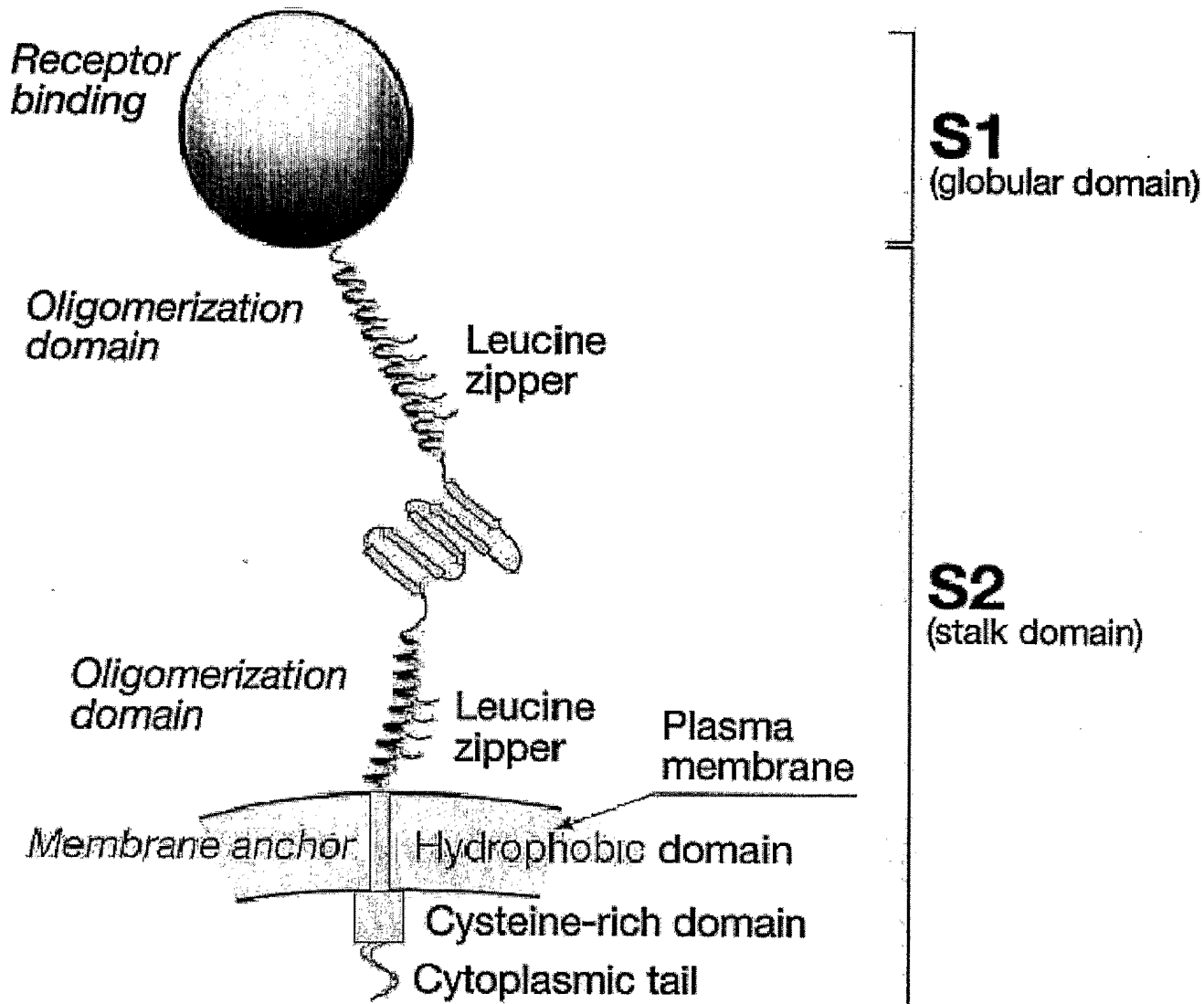
FIGURE 19**FUNCTION****STRUCTURE**

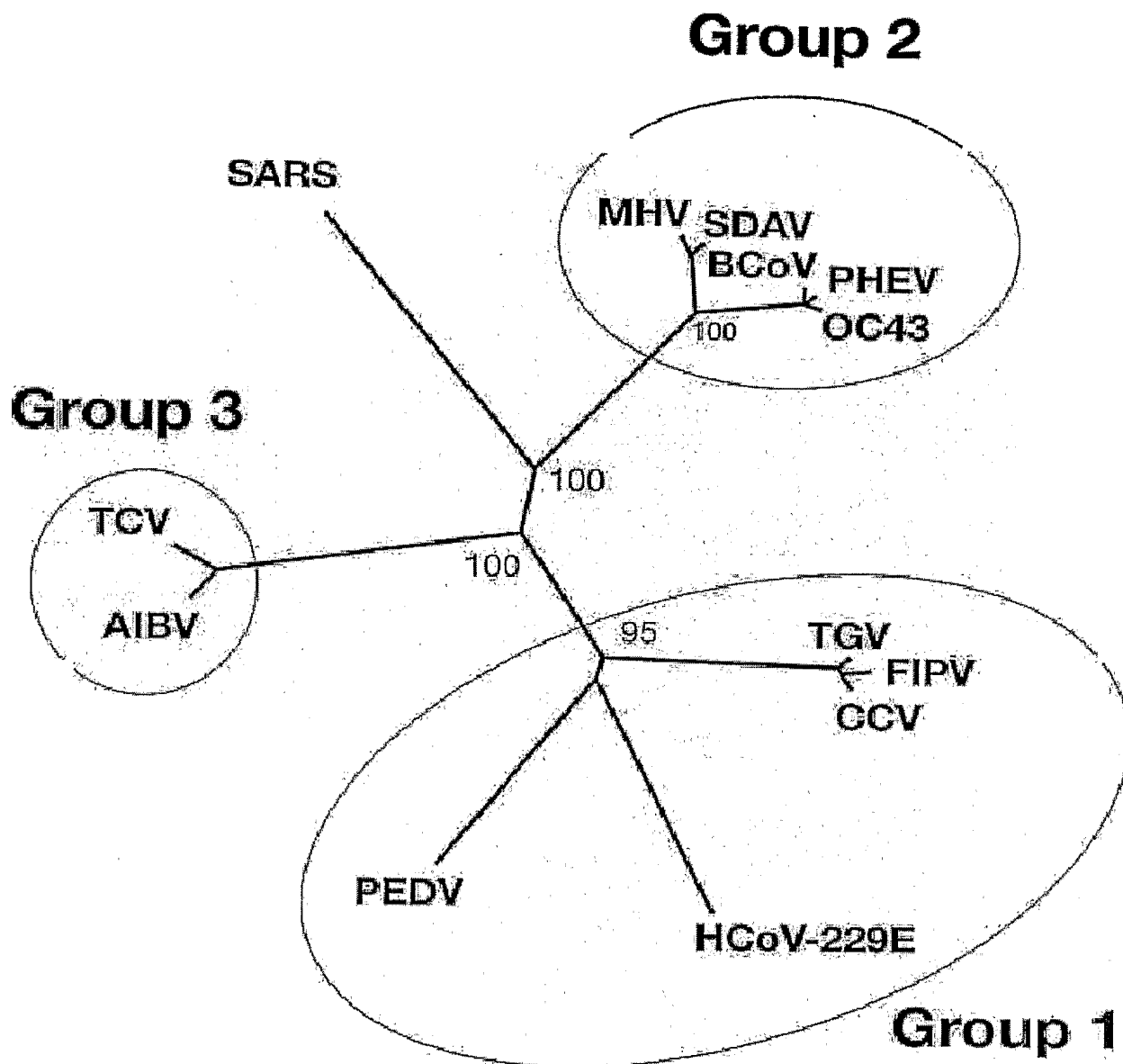
FIGURE 20

FIGURE 21

FIGURE 21A

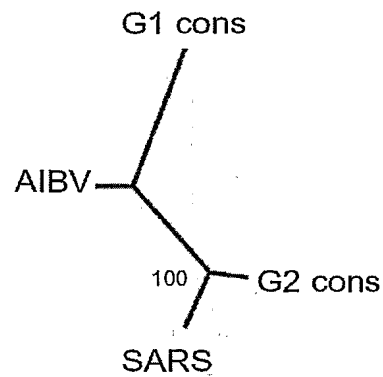


FIGURE 21B

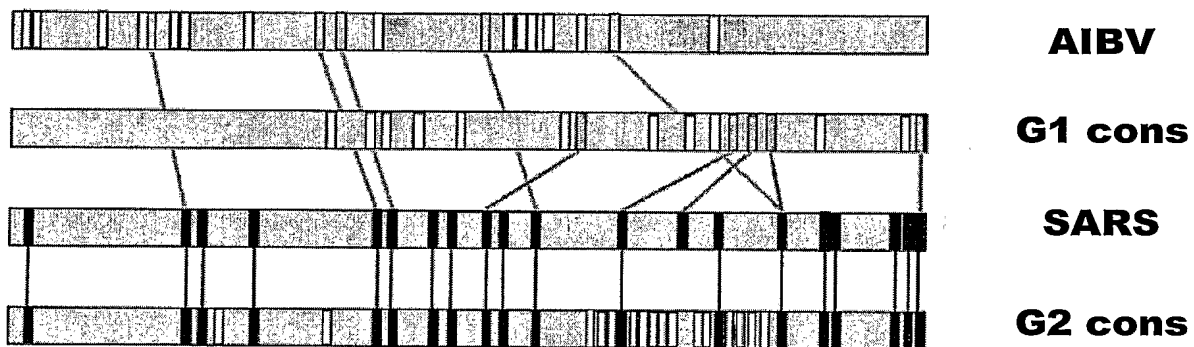


FIGURE 22

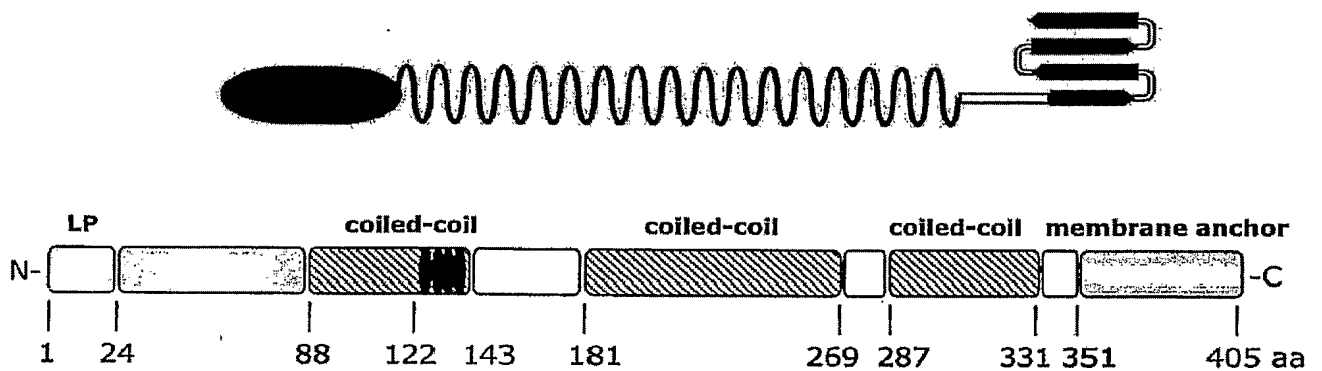


FIGURE 23

LPRKSQPTSIISCRSVL-TNFKICVAVARLHA-CTYAV-TIINF TVVDKKRVTRPSSADCL
 RFRPCCSRSSAYLGFVRV-PKGKMESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVEE
 ALSEAREHLKNGTCGLVELEKGVLPQLEQPYVFIKRSDALSTNHGHKVVELVAEMDGIQY
 GRSGITLGLVLPVHVGETPIAYRNVLLRKNGNKGAGGHSYGIDLKSYDLGDELGTDPIDY
 EQNWNTKHGSGALRELTRELNGGAVTRYVDNNFCGPDGYPLDCIKDFLARAGKSMCTLSE
 QLDYIESKRGVYCCRDHEHEIAWFTERSDKSYEHQTPFEIKSAKKFDTFKGECPKFVFPL
 NSKVKVIQPRVEKKKTEGFMGRIRSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFL
 KATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHNSNIETRL
 RKGGRTRCFGGCVFAYVGCYNKRAYWVPRASADIGSGHTGITGDNVETLNEDLLEILSRE
 RVNINIVGDFHLNEEVAILASFSASTSFAIDTIKSLDYKSFKTIVESCNGYKVTKGKPV
 KGAWNIGQQRSVLTPLCGFPSQAAGVIRSIFARTLDAANHSIPDLQRAAVTILDGISEQS
 LRLVDAMVYTSDLLTNSVIIMAYVTGGLVQQT SQWLSNLLGTTVEKLRPIFEWIEAKLSA
 GVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVKCFIDVVNKALEMCIDQVTIAG
 AKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVTFLEGDSHDTVLTSEEVV
 LKNGELEALETPVDSFTNGAIVGTPVCVNGLMLEIKDKEQYCALSPGLLATNNVFRKLG
 GAPIKGVTFGEDTVWEVQGYKNVRITFELDERVDKVLNEKCSVYTVESGTEVTEFACVVA
 EAVVKTLQPVSDLLTNMGIDLDEWSVATFYLFDDAGEENFSSRMYSFYPPDEEEEDDAE
 CEEEEIDETCEHEYGTEDDYQGLPLEFGASAETVRVEEEEEEDWLDDETTTEQSEIEPEPEP
 TPEEPVNQFTGYLKLTDNVAIKCVDIVKEAQSANPMVIVNAANIHLKHGGGVAGALNKAT
 NGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVVGPNL NAGEDIQLLKAAYENFN
 SQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQVYIAVNDKALYEQVVM DYLDNLKPRVE
 APKQEEPPNTEDSKTEEKSVVQKPVDVKPKIKACIDEVT'TTLEETKFLTNKLLLFADING
 KLYHDSQNMLRGEDMSFLEKDAPYMGDVITSGDITCVVIPS K KAGGTTEMLSRALKKVP
 VDEYIT'TYPGQGCAGYTLEEAKTALKKCKSAFYVLPSEAPNAKEEILGTVSWNLREMLAH
 AEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRRFFFYTSKEPVASII'TKLNLSL
 NEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAVVSVSSPD AVT'TYNGYLTSSSKTSEEHF
 VETVSLAGSYRDWSYSGQRTTELGVFLKRGDKIVYHTFLES PVEFHLDGEVLSLDKLSLL
 SLREVKTIKVFT'TVDNTNLHTQLVDMSMTYGGQFGPTYLDGADVTKIKPHVNHEGKTFV
 LPSDDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWKFPQVGGLTSIKWADNNCYLSSVL
 LALQQLEVKF NAPALQEAYYRARAGDAANFCALILAYS NKT V GELGDVRETMT HLLQHAN
 LESAKRVLNVVCKHCGQKTT'TLTGVEAVMYMGTL SYDNLKTGVSIPCVCGRDATQYLVQQ
 ESSFVMM SAPP AEYKLQQGTFLCANEYTGNYQCGHYTHITAKETLYRIDGAHLTKMSEYK
 GPVTDVIFYKETS YTTTIKPVSYKLDGVTYTEIEPKLDGYKKDNAYYTEQPIDLVPTQPL
 PNASFDNFKLTCSNTKFADDLNQMTGFTK PASRELSVTFFPDLNGDVVAIDYRHYSASF
 KGAKLLHKPIVWHINQATTKTTFKPNTWCLRLWSTKPVDT SNSFEVLAVEDTQGM DNLA
 CESQQPTSEEVENPTIQKEVIECDVKTTTEVVG NVILKPSDEGVKVTQELGHEDLMAAYV
 ENTSITIKKPNELSLALGLKTIATHGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRL
 AQRVFNNYMPYVFTLLFQLCTFTKSTNSRIRASLP TTI AKNSVKSVAKLCLDAGINYVKS
 PKFSKLFTIAMWLLLLSICLGLSICVTAAFGVLLSNFGAPS YCNGVRELYLNSSNVTTMD
 FCEGSFPCSI CLSGLDSLDSYPALETIQVTISSYKLDLTILGLAAEWV LAYMLFTKFFYL
 LGLSAIMQVFFGYFASHFISNSWLMWFIISIVQMAPVSAMVRMYIFFASFYIWKSYVHI
 MDGCTSSTCMMCYKRN RATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDT FCT
 GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVAVKNGALHLYFDKAGQKTYERHPLSH
 FVNLDNLRANNTKGSLPINVIVFDGKSKCDESASKSASVYYSQ LMCQPIILLDQALVSDV
 GDSTEVS VKMFDAYVDTF SATFSVPMEKLKALVATAHSELAKGVALDGVLSTFVSAARQG
 VVDTDVDTKDVIECLKLSHHS DLEVTDGSCNNFMLTYNKVENMTPRDLGACIDCNARHIN
 AQVAKSHNVSLIWNVKDYMSLSEQLRKQIRSAAKNNIPFRLTCATTRQVNVNITTKISL
 KGGKIVSTCFKLMLKATLLCVLAALVCYIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDI
 ISTDDCFANKHAGFDAWFSQRGGSYKNDKSCP VVAAIITREIGFIVPGLPGTVLRAIN GD
 FLHFLPRVFSAVGNICYTPSKLIEYSDFATSACVLAAECTIFKDAMGKVPYCYDTN LLE
 GSISYSELRPDTRYV LMDGSIIQFPNTYLEGSVRVVTTFDAEYCRHGT CERSEVGICLST
 SGRWVLNNEHYRALSGVFCGVDAMNLIANIFTPLVQPVGALDVSASV VAGGIIAILVTCA
 AYYFMKFRRVFGEYNHVVAANALLFLMSFTILCLVPAYSFLPGVYSVFYLYLTFYFTNDV
 SFLAHLQWFAMFSPIVPFWITAIYVFCISLKHCHWFFNNYLRKRVMFNGVTFSTFEEAAL

CTFLLNKEMYLKLRSETLLPLTQYNRYLALYNKYKYFSGALDTTTSYREAACCHLAKALND
FNSNGADVLYQPPQTSITSAVLQSGFRKMAFSPSGKVEGCMVQVTCGTTTTLNGLWLDDTVY
CPRHVICTAEDMLNPNYEDLLIRKSNHSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPK
TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNHTIKGSFLNGSCGSGVGFNIDYDCV
SFCYMHMELPTGVHAGTDLEGKFYGPVDRQTAQAAGTDTTITLNVLAWLYAAVINGDR
WFLNRFTTTLNDFNLVAMKYNIEPLTQDHVDILGPLSAQTGIAVLDMCAALKELLQNGMN
GRTILGSTILEDEFTPFDDVVRQCSGVTFQKGFKKIVKGTHHWMLLTFTLSLLILVQSTQW
SLFFFVYENAFLEPFTLGIMAIAACAMLLVKHKHAFLECLFLLPSLATVAYFNMVYMPASWV
MRIMTWLELADTSLSGYRLKDCVMYASALVLLILMTARTVYDDAARRVWTLNMVITLVYK
VYYGNALDQAI SMWALVISVTSNYSYSGVVTTIMFLARAI VFCVEYYPLLFITGNTLQCIM
LVYCF LGYCCCCYFGLFCLLNRYFRLTLGVYDYL VSTQEFYRMYNSQGLLPKSSIDAFKL
NIKLLGIGGKPCIKVATVQSKMSDVKCTSVVLLSVLQQLRVESSSKLWAQCVQLHNDILL
AKDTTEAFEFKMSVLLSVLLSMQGAVDINRLCEEMLDNRATLQAIASEFSSLPSYAAAYATA
QEAYEQAVANGDSEVVLLKKLKKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYKQARSED
KRAKVT SAMQTMLEF TMLRKLND DALNNI INNARDGCVPLNII PLTTAAKLMVVVPDYGT
KNTCDGNTFTYASALWEIQQVVDADSKIVQLSEINMDNSPNLAWPLIVTALRANSVAVKLQ
NNELSPVALRQMSCAAGTTQTACTDDNALAYNNSKGGFRVLALLSDHQDLKWARFPKSD
GTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGLNNLNRGMVLGSLAATVRLQAGNATEV
PANSTVLSFCAFAVDPKAYKDYLASGGQPI TNCVKMLCTHTGTGQAITVTPEANMDQES
FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRNTVCTVCGMWKGYG
CSCDQLREPLMQSADASTFLNGFAV-VQPV LHRAAQALVLMSSSTGLLIFTTKKLLVLQSS
-KLI AVASRRRMRKAIY-TLTL-LRGILCLT TNMKRLFITWLKIVQRLLSMTFSSLE-MV
TWYHIYHVS-VNTQWLI-SMLYVILMRVIVIH-KKYSSHTIAVMMIISIRRIGMTS-RI
LTSYAYMLT-VSVYANHY-RLYNSAMLCVMQAL-AY-H-IIRILMGTGTISVISYK-HQA
AEFLLEWIHITHC-CPSSL-LGHWLLSPIWMLISQNHLLSGIC-NMILRKRDFVSSTVILN
IGTRHTIPIVLTVMIGVSFIVQTLMCYFLLCFHLQVLDH--EKYL-MVFLLLFQLDTIF
VS-ESYIIRM-TYIARVS VSRNF-CMLLIQLCMQLLAIYC-INALHAFQ-LH-QTMLLFK
LSNPVILIKTFMTLLCLKVSLRKEVLLN-NTSSLLRMATLLSVIMTIIVIICQQCVISDN
SYS-LKLLINTLIVTMVAVLMPTK-SLTIWINQLVSHLINGVRLDFIMTQ-VMRIKMHFS
RILSVMSLL-LK-ILSMPLVQRIELAP-LVSLSVVL-QIDSFIRNY-SQ-PPLEELLW-
LEQASFTVAGIIC-KLFTVM-KLHTLWVGIIQNVTEPCLTCLG-WPLLFLLANITLAVTY
HTVSTG-LTSVRKY-VRWSCVAAHYMLNQVEHHPVMLQLLMLIVSLTFVKLLQPM-MHFF
QLMVIR-LTSM SAIYNTGSM SVSIEIGMLIMNSWMSFTLT CVNISP--FFLMPLCAITV
TMRLKV--LALRTL RQFFIIKIMCSCLRQNVGLRLTLLKDLTNFAHSIQC-LNKEMITCT
CLTQIHQEY-AQAVLSMILSKQMVHL-LKGSCHWLLMLTHLQNILIRSMMSFTCIYNTL
ESYMSLLATCWTICIP-C-LMITPHGTGNLSFMRLCTHHIQSCRL-VLVYCAIHR LHFVA
VPVLGDHSYVASAAMTMSFQHHTN-CCLLIPMFAMPQVVM SLM-HNCI-EV-AIIASHIS
LPLVFHYVLMVRFLVYTKTHV-AVTMSLTSMR-QHVI GLMLAITYLPTLVLRDSSFSQQK
RSKPLRKHLSCHMVLPLYAKYSLTENCIFHGRL ENLDHH-TETMSLLVTV-LKIVKYRLE
STPLKKVTMVMLLCTEVL RHTS-MLVITLC-HLTL-CHLVHLL-CHKSTM-ELLACTQHS
TSQMSFLAMLQIIKRSACKSTLHSHKDLVLVRVILPSDLLSITHLLA-CIRHALMQLLMP
YVKRH-NICP-INVVESYLRVRA-SVLINSK-IQH-NSMF SAL-MHCQKQLLTL-SLMKS
LWLLIMT-VLSMLDFVQNTTSILAILLNYQPPAHC-LKAH-NQNILIQCADL-KQ-VQTC
SLELVAVVLLKLLTL-VL-FMTIS-KHTRISQLNASKCSTKVLLHMMFHLQSTD LK-AL-
ENFLHAILLGEKLF LSHLIIHRTL-LQKS-DCLRLLIHRVLNMTMSYSHKLLKQHTLV
MSTASMWLSQGQKLAFCA-CLIEIFMTNCNLQV-KYHVAMWLHYKQKM-LDFLRTVVRSL
LVFILHRHLHTSALI-SSRLKDYVLTYQAYQRT-PTVDSSL-WVSK-ITKSMVTLICLSP
AKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPE
LMQNLHQVTSNLILYHSCIKACPGM-CVLR-YKCSVIH-KDCQTESC SSGRMALSLHQ-
STLSRLDLKERVVCVTNVQLAFL LHQILMPAGIILWVLTMSITHL-LMFSSGALRVTFRV
TMTNIARYMEMHMLVVM LS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLA EKYNTW
L-SLHCLLISFQFFMTLEIQR LSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILMLHITI
NSLMVFVCFGIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVVC M-ISMHSTLQLSIKVH
LLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VVLFADTMQMSTDSTW
MHII--FLLDLAYGFTNNLILITCGIHLPGYRV-KMWLIMLLIKD TLM DTPAKHLFP SLI
MLFTQR-MVLMWRS LKIRQHFLMLHL SFGLSVTLNQCQR LRSIIWVLISLLIL-SGTT

KEKPQHMYLQ-VSAQ-LTLPRNLLRVLVLHLLSCLMVWVKDR-TFLET PVMVF--QKVQS
KV-HLQORDQHKLASMESH-LENQ-KHSLTTLRK-TALFNSCLKPTLLRAET-RILSPDHK
WKLTFSSSLWMNSYSDISSRAMPSNTSFMEISVMDNLAVFI---A-PSAHKIHHLN-RIL
SLWTAQ-KITS-QMRKQVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFH
SCFGVRMDMLKPSTQNYKQVERGNQVLRCLTCTRCKEFLKSVTFRIMVKMLLYQKE---
MSQSILNCVNT-IHLL-LYPTT-ELFTLVLALIKELHQVQLCSDNGCQLAHYLSIQILMT
SSPTHILL-LETVQQYIRLINGTLLLAICMTLGPNM-QKRMTLKKGFSLICVDL-SKN-P
WVVL-L-R-QSILGMLTFTSLWAISHGGQLLQOM-MHHHRKHF-LGLTILASRRNKLMAI
PCMLTTFSGGTQILSSCLPIHSLT-ANFLN-EELL-CLLRRIKSMI-FILFWKKVGLSL
EKTTELWFQVIFLLTTKRTCLFSYYFLLSLVVVTLTGAPLLMMFKLLITLNLHL-GGFT
ILMKFLDQTLFI-LRIYFFHFILMLQGFILLIIRLATLSYLLRMVFIILLPQRNQMLS VVG
FLVLP-TTSHSR-LLLTILLMLLYEHVTLNVCVTTL SLLFLNPWVHRHIL-YSIMHLIALS
STYLMPPFRMLFQKSQVILNTYESLCLKIKMGFSMFIRAINL-M-FVIYLLVLT-LNFLS
CLLVLTQLILEPFLQPFHLLKTFGARQLQPILLAI-SQLHLCSSMMKMVQSQMLLIVLKI
HLLNSNALLRALRLTKEFTRPLISGLFPQEML-DSLILQTCVLLERFLMLLNSLLSMHGR
EKKFLIVLLITLCSTTQHFFQPLSAMAFLPLS-MIFASPM SMQILL-SREMM-DK-RQDK
LVLLLI I I I INCQMISWVVSLLGILGTLMMLQLVII I I INIGILDMASLGPLRETYLMCLSP
LMANLAPHLLLLIVIGH-MIMVFTPLLALATNLTEL-YFLLNF-MHRPRFVDQNYPLTLLR
TSVSILILMDSLVLVC-LLLQORDFNHFNNLAVMFLISLIPFEILKHLKY-TFHLALLGV-
V-LHLEQMLHLKLLFYIKMLTALMFLQQFMQINSHQLGAYILLETMYSRLKQAVL-ELSM
STLLMSATFLLELAFVLVTIQFLYVVLAKNLLWLILCL-VLIVQLLTITPLLYLLTFQ
LALLQK-CLFLWLKPP-IVICTSAEILLNVLICFSNMVAFAHN-IVHSQVLLLNRIATHV
KCSLKS NKCTKPQL-NILVVLIFHKYYLTL-SQLRGLLLRTCSLIR-HSLMLAS-SNMAN
A-VILMLEISFVRRSSMDLQCCHLCSLMI-LLPTLLL-LVVLPLLDGHLVLALLFKYLLL
CKWHIGSMALELPKMF SMRTKNKSPTNLTRRLVKFKNHLQQHQLHWASCKTLLTRMLKH-
THLLNNLALILVQFQVC-MISFRDLIKSRRRYKLTG-LQADFKAFKPM-HNN-SGLLKSG
LLLILLLLKCLSVFLDNQKELTFVERATTLCPSHKQPRMVLSSYMSRMCHPRRGTS PQRQ
QFVMKAKHTSLVKVFLCCLMALLGLLHRGTSFLHK-LLQTIHLSQEIVMSLLASLTQFMI
LCNLSLTHSKKSWTSTSKI IHHQMLILATFQALTLLSSTFKKKLTASMRSLKI-MNHSLT
FKNWENMSNINLGLGMFGSASLLD-LPSSWLQSCFVA-LVVAVASRVHALVVLAASLMRM
TLSQFSRVSNYITHKRTYGFVYEIFYSWINYCTASKN-QCFSCKYCSCYSNDTATSLTPF
RMACYWRCISCCFSERYQNNCAQ-KMAASPL-GLPVHLQFTAAICYHLFTSFACRCRYGG
AIFVPLCLDIFSTMHORM-NYYEMLALLEVQIQEPITL-CQLLCLLAHT-L-LLYTI-QC
HRYNCRY-R-RHFNTKTQRRLPNWWLF-G-ALRC-RLCRCTWLFHRSLLPA-VYTNYRHR
WY-KCYILHL-QAC-RPTECANTHNRRLFRSC-SSNGSNL--ADDDY-RAFVSTRK-VRT
YVLIRFGRNRYVNS--RTSFSCFRGILASHTSHPYCASIVCVLLQYC-REFSKTNGLRLL
AC-KSELF-RSS-SSGLNELTII I I I LFGTLTLLIMADNGTITVEELKQLLEQWNLVIGFL
FLAWIMLLQFAYSNNRNLFLYII I I I KLVLFWLLWPVTLACFVLA AVYRINWVTGGIAIAMACI
VGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLRGITVTRPLMESELVIGAVIIRG
HLRMAGHSLGRCDIKDLPKEITVATSRTLSYYKLGASQRVGTD SGFAAYNRYRIGNYKLN
TDHAGSNDNIALLVQ-VTTDVSSC-LPGYNSRDIDYHYEDFQDCYLES-RYNKFNSETII
-ASN-EELFGVR--RTYGVRLSIKRT-KLFSS-H-LYLHLASYITIRSVLEVRLYY-KNL
AHQEHTRAIHFTLLLTINLH-LALAHTLLLLVLTVLDIPISCVQDQFHQNFSSDKRRFN
KSSTRHFFSLLLL-YF-YFASPLRERQNE-AHFN-LLFVLFSLSAIPCFNNAYYILVFTR
NPGSRRTLYQSLNEHETSHCFDLYFSMQLHMH CSTALCI--TSCA-RSL-GTTLGVLIIA
LLGFVL-ERFYLFIDGTLWFKHAHMLLSTVKIQLVVRL-LGVGTFMKVTKLLHLETYLL
F-INEQIKMSDNGPQSNQRSAPRITFGGPTDSTDNNQNGRNGARPKQRRPQGLPNNTAS
WFTALTQHGKEELRFPRGQGVPI NTNSGPDDQIGYYRRATRVRVGGDGKMKELSPRWYFY
YLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVQLPQGTTL PKGF
YAEGSRGGSQASSRSSRSRGNSRNSTPGSSRGNSPARMASGGGETALALLLLDRLNQLE
SKVSGKGQQQQGQTVTKKSAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDL
IRQGTDYKHWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVI
LLNKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLPAADMDDFSRQLQNSM
SGASADSTQA-TLMMTTQGRWAM-TFSQFRLRYIVYSCAE-ILVTKQHK-V-LTLISHSN
L-SMCNIREDLKEPPHFHRGHAEYDRGYSE-C-GELPIWKSPNV-N-F-CYPHVILIAS

FIGURE 24

TQEKPTNLDLL-ICSLNEL-NLCSCRSAACLVHLRSINNNKFYCR-QETSNSSLFCRLLT
VSSVLQSIISIPRFRPGVTER-DGEPCSWCQRENTTRPTQFACPSG-RRASAWLRGLCGRG
PIGGT-TPQKWLWSSRAGKRRTAPA-TALCVH-TF-CLKHQSRPQGR-AGCRNGRHSVR
S-RYNTGSTRATCGRNPNCIPQCSSS-ER--GSRWS-LWHRSKVL-LR-RAWH-SH-RL-
TKLEH-AWQWCTP-THS-AQWRCSHSLCRQQFLWPRWVPS-LHQRFSTRTRGQVNVHSFRT
T-LHRVEERCLLLLP-P-A-NCLVH-AL--ELRAPDTRLN-ECQEI-HFQRGMPKVCVSS-
LKSQSHSTTC-KEKD-GFHGAYTLCVPCCISTGV-QYALVYLDLDEM-SLR-SFMADVRLSE
SHL-TLWH-KFSY-RTYYMWVPTY-CCSENAMSCLSRPRDWT-A-CCRLSQPLKH-NSTP
QGR-D-MFWRLCVCLCWLL--ACLLGSSC-C-YWLRPYWHYW-QCGDLE-GSP-DTES-T
C-H-HCWRFSE-EGCHHFGIFLCFYKCLY-HYKES-LQVFQNH-C-VLR-L-SYQGKARK
RCLEHWTTEISFNTTVWFSLTGCWCYQINFCAHT-CSKPLNS-FAKSSCHHT-WYF-TVI
TSCRRHGLYFRPAHQQCHYYGICNWWSCCTTDFSVVV-SFGHYC-KTQAYL-MD-GET-CR
S-ISQGCGLGDSQISHYRCF-HRQGSNTGCFR-HQGLCKMLH-CC-QGTRNVH-SSHRYWR
KVAITQLR-SLHRSKQGTLPVYTWQGAATTHAS-GTKRSNLS-R-FT-HSTYL-GGCS
QER-TRSTRDAR--LHKWSYRRHTSLCKWPHALRD-GQRTILRIVSWFTGYKQCLSLKRG
CTN-RCNLWRRYCLGSSRLQECENHI-A--TC-QSA--KVLCLHC-IRYRSY-VCMCSSR
GCCEDFTTSF-SPYQHGYS--VECSYILLI--CW-RKLFITYVLFLLPSR-GRRGRCRV
-GRN--NL-T-VRYRG-LSRSPSGIWCLS-NSSS-GRRRGRLAG-YY-AIRD-ARTRTY
T-RTS-SVYWLKTY-QCCH-MC-HR-GGTKC-SYGDCKCC-HTPETWWWCSRCTQQGNQ
WCHAKGE--LH-AKWPSYSRRVLFAPWT-SC-EVSACCWT-PKCR-GHPAS-GSI-KFQF
TGHLTCTIVVSRHIWC-TTSVFTSVRADGSYTGLYCSQ-QSSL-AGCHGLS--PEA-SGS
T-TRGATKHRRFQ-GEICRTEACRCEAKN-GLH--GYHNTGRN-VSYQ-VTLVC-YQW-
ALP-FSEHA-R-RYVFP-EGCTLHGR-CYH-W-YHLCCNTLQKGWWHY-DALKSFEEAS
--VYNHVPWTRMCWLYT-GS-DCS-EMQICILCTTFRST-C-GRDSRNCILEFERNACSC
-RDKKINAYMHGC-SHNGNHPT-V-RN-NSRGHR-LWCPILLY--RACSFYYYEAEISK
-AACHNANWLCDTWF-S-RGCALYAFS-SSCRSVSIITRCCYYI-WIPHFVIKDI-GALC
RNSFFGWLLQRLVLFRTAYRVRC-IS-AW-QNCVPHSGEPRRVSS-R-GSFT-QTKESLI
PAGG-DYKSVHNCGQH-SPHTACGYVYDIWTAVWSNILGWC-CYKN-TSCKS-G-DFLCT
T--HTT--SFRVLPYS--EFSW-VHVCFKPHKEMEISSSWWFNFN-MG--QLLFV-CFI
STSTA-SQIQCTSTSRGLL-SPCW-CC-LLCTHTRLQ--NCWRAW-CQRNYDPSSTAC-F
GICKASS-CGV-TLWSENYLNGCRSCDVYGYSL--S-DRCFHSMCVWS-CYTISSTTR
VFFCYDVCTTC-V-ITARYILMCE-VHW-LSVWSLHSYNC-GDPLSY-RSSPYKDVRVQR
TSD-CFLQGNILHYNHQACVV-TRWSYLHRD-TKIGWVL-KG-CLLYRAAYRPCTNSTIT
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-KSTTHL-RSSGKSYHTEGSHRV-RENYRSCRQCHT-TIR-RC-SNTRVRS-GSYGCLCG
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GWLHLFDLHDVL-AQSCHTR-VYNYC-WHEEIFLCLCKWRPWLLQDSQLELSQL-HILHW
-YIH--SCS-FVTPV-KTNQPY-PVIVYC--CCCEKWRASPLL-QGWSKDL-ETSALPF
CQFRQFES-QH-RFTAY-CHSF-WQVQMRRVCF-VCFCVLQSAADVPTYVA-PSSCIRRW
R-Y-SFR-DV-CLCRHLFSNF-CSYGKT-GTCCYSSQRVSKGCSFRWCIFYIRVSCPTRC
C-YRC-HKGCY-MSQTFTSL-LRSDR-QL-QFHAHL--G-KHDAQRSWRMY-L-CKAYQC
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GW-DC-YLF-TYA-GHIIVRSCCIGLLYRYASTYIVNP-WLHK-NHWLQSHSGWCHS-HH
FY--LFCK-TCWF-RMV-PAWWFIQK-QKLPCSSCYHYKRDWFHSAWLTGYCAESNQW-L
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CQFNCAFLLCFCSRPC-SI-GLPSKWRTTNHQLCEDVVYTHWYRTGNYCNTRS-HGPRVL
WWCFMLSVL-MPH-PSKS-RIL-LER-VRPNTYHLC--PSGFYT-KHSLYRLRNVERLWL
-L-PTPRTLDVCGCINVFKRVCVSAARLTPCGTGTSTDVVYRAFDIYNEKVAGFAKFL
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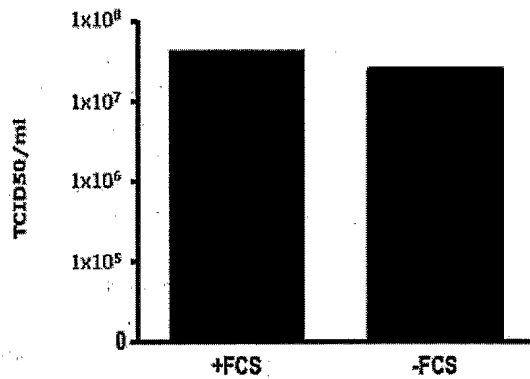
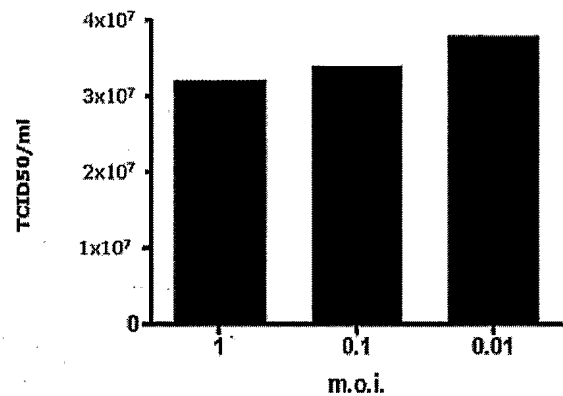
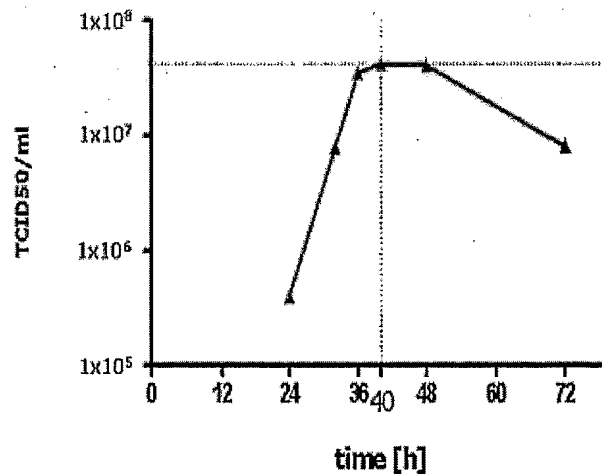
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FIGURE 25

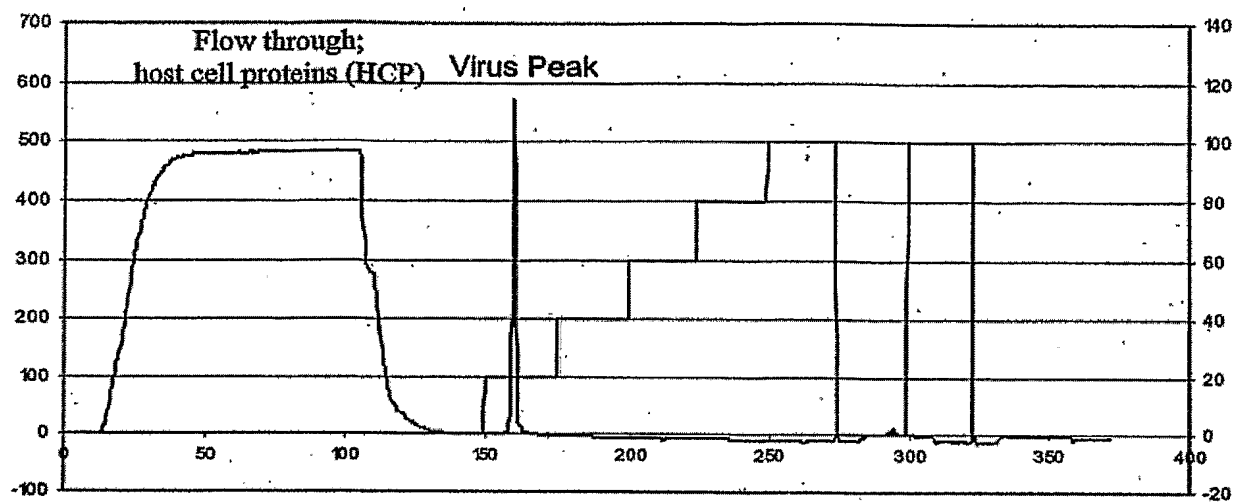
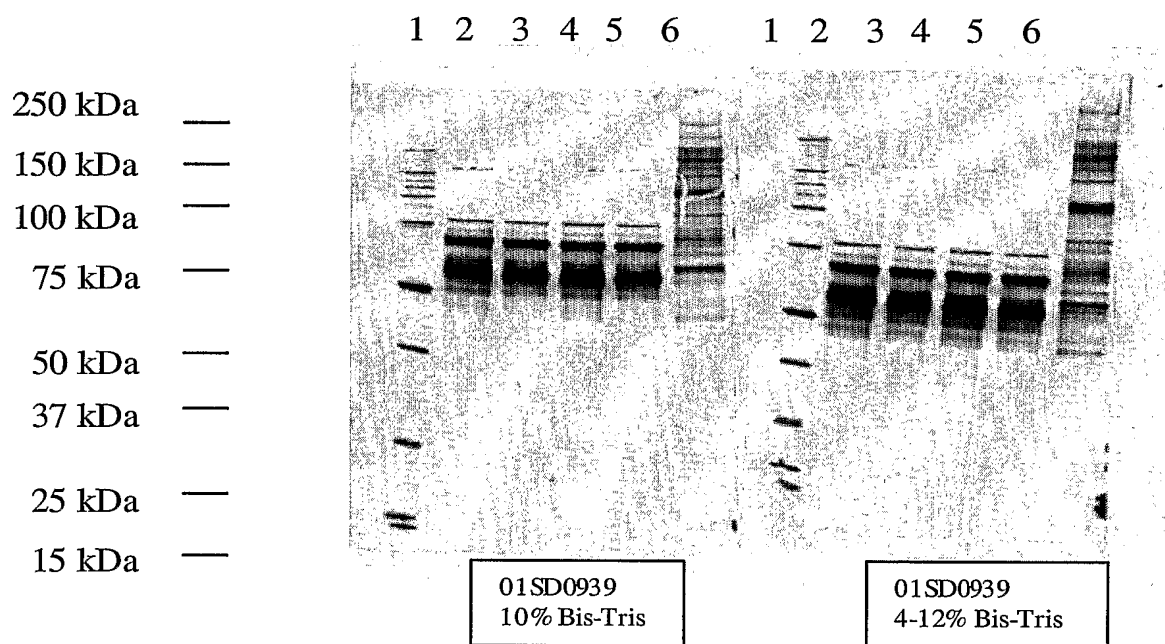
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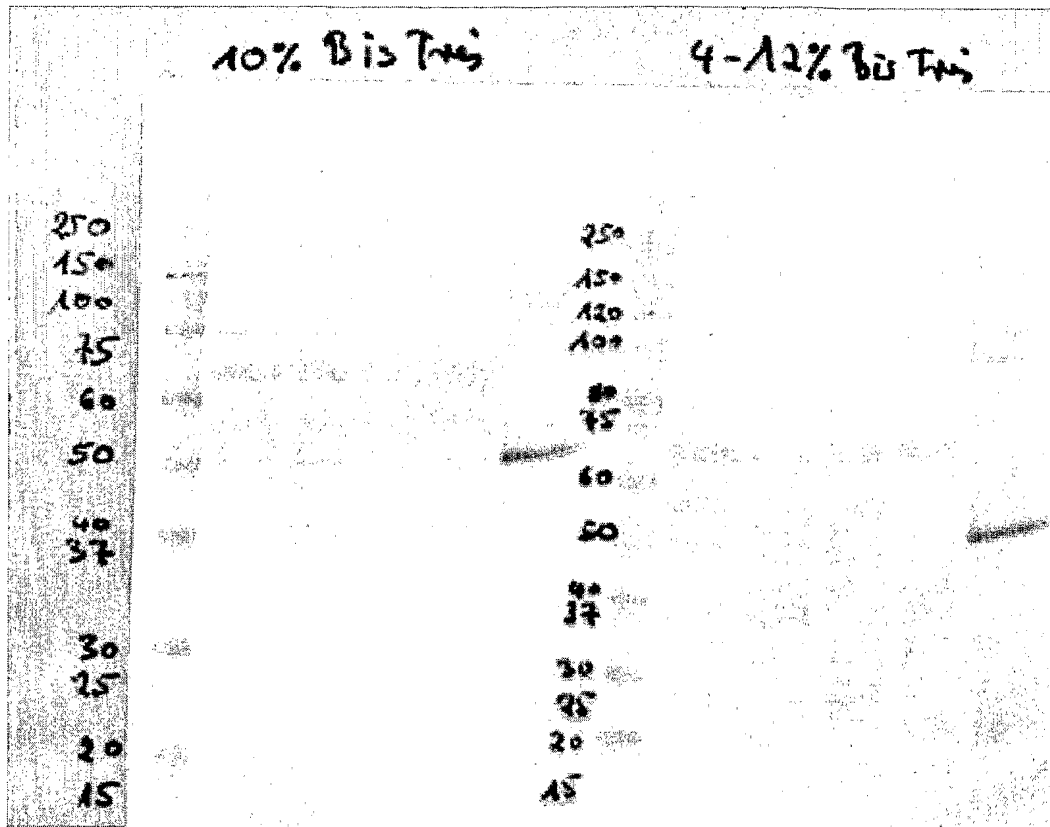
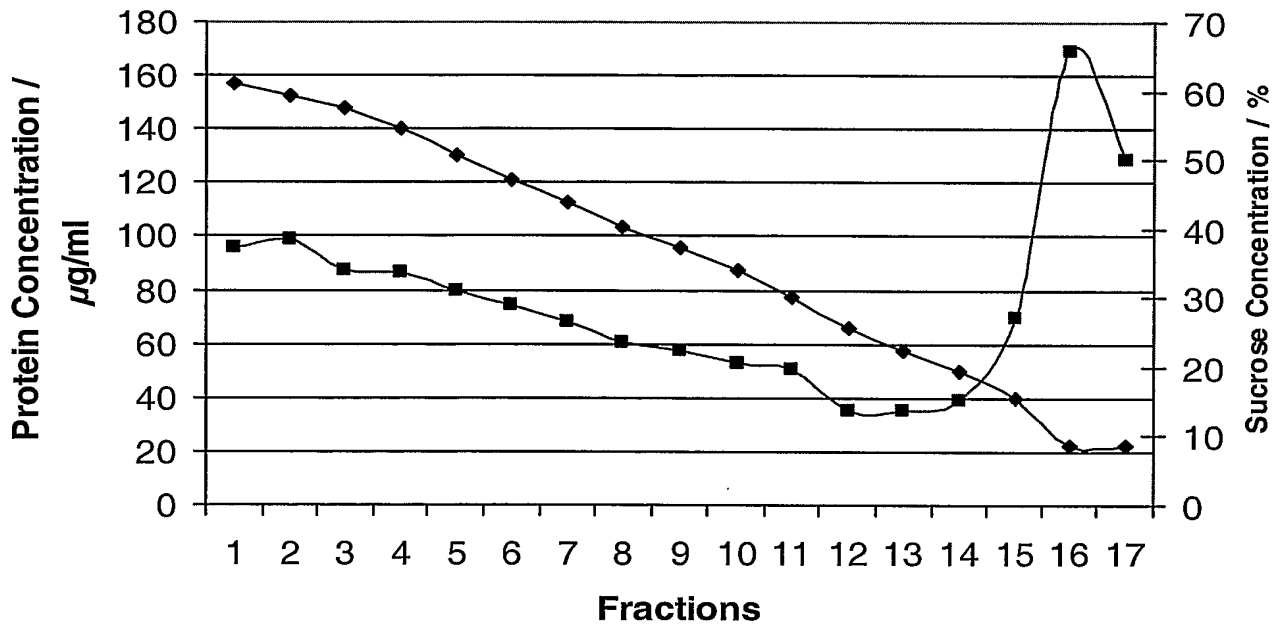
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FIGURE 26**FIGURE 26A****FIGURE 26B****FIGURE 26C**

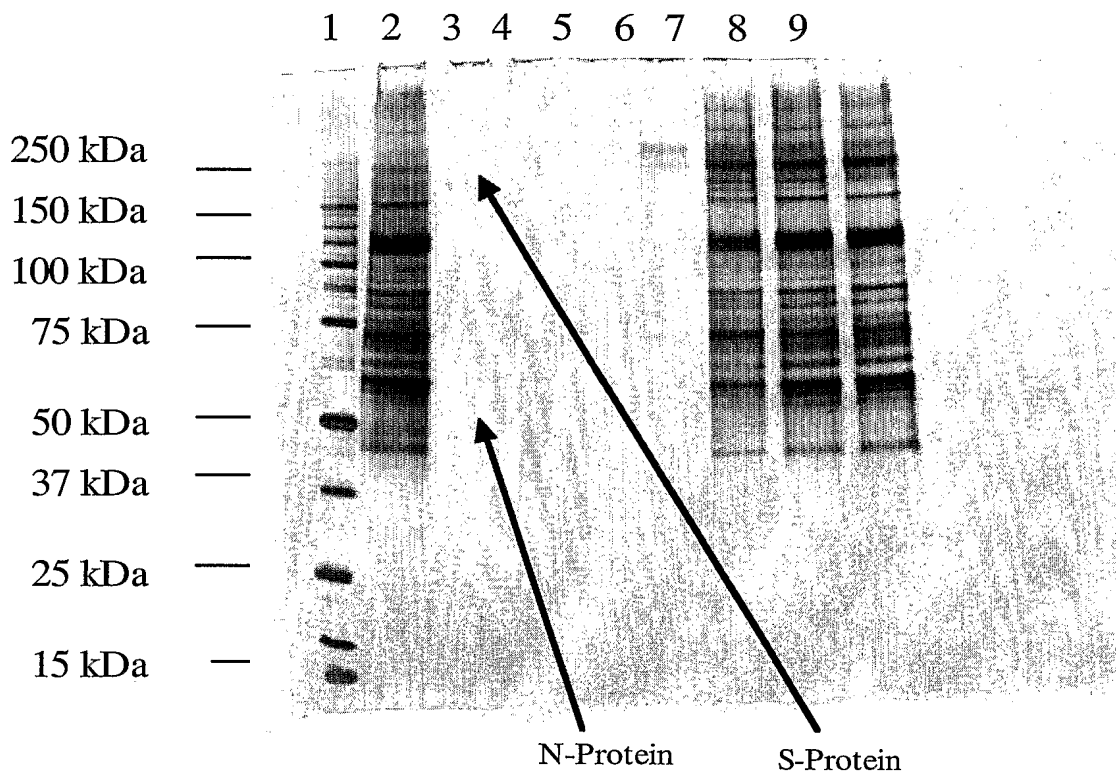
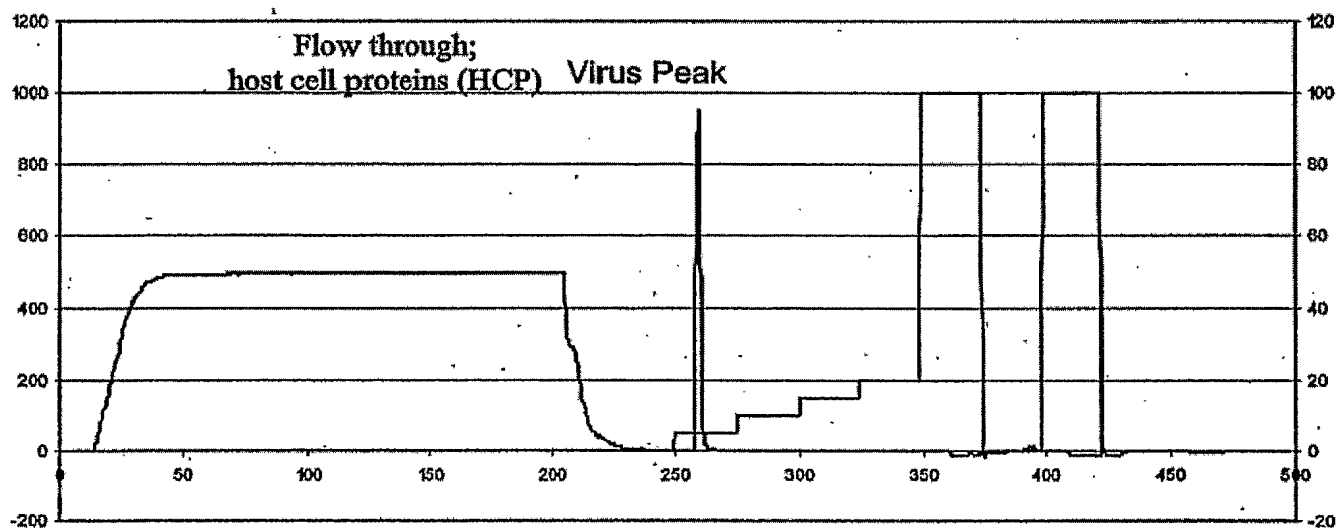
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FIGURE 27**FIGURE 28**

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FIGURE 29**FIGURE 30**

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FIGURE 31**FIGURE 32**

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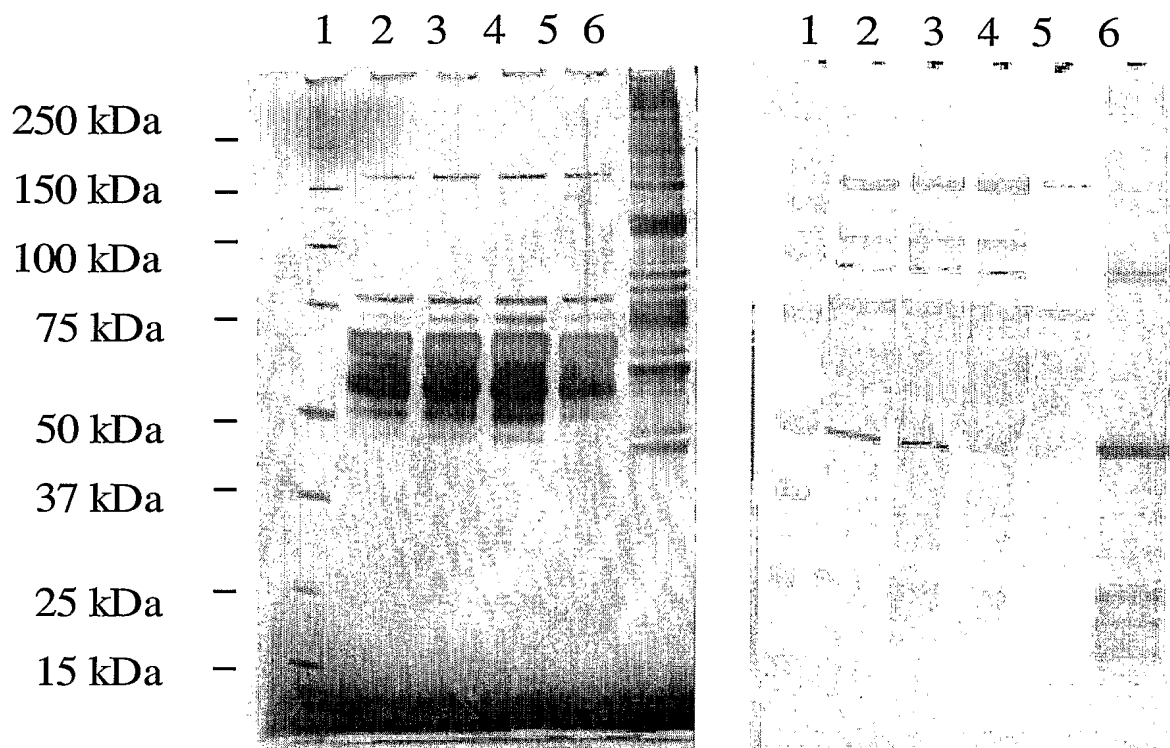
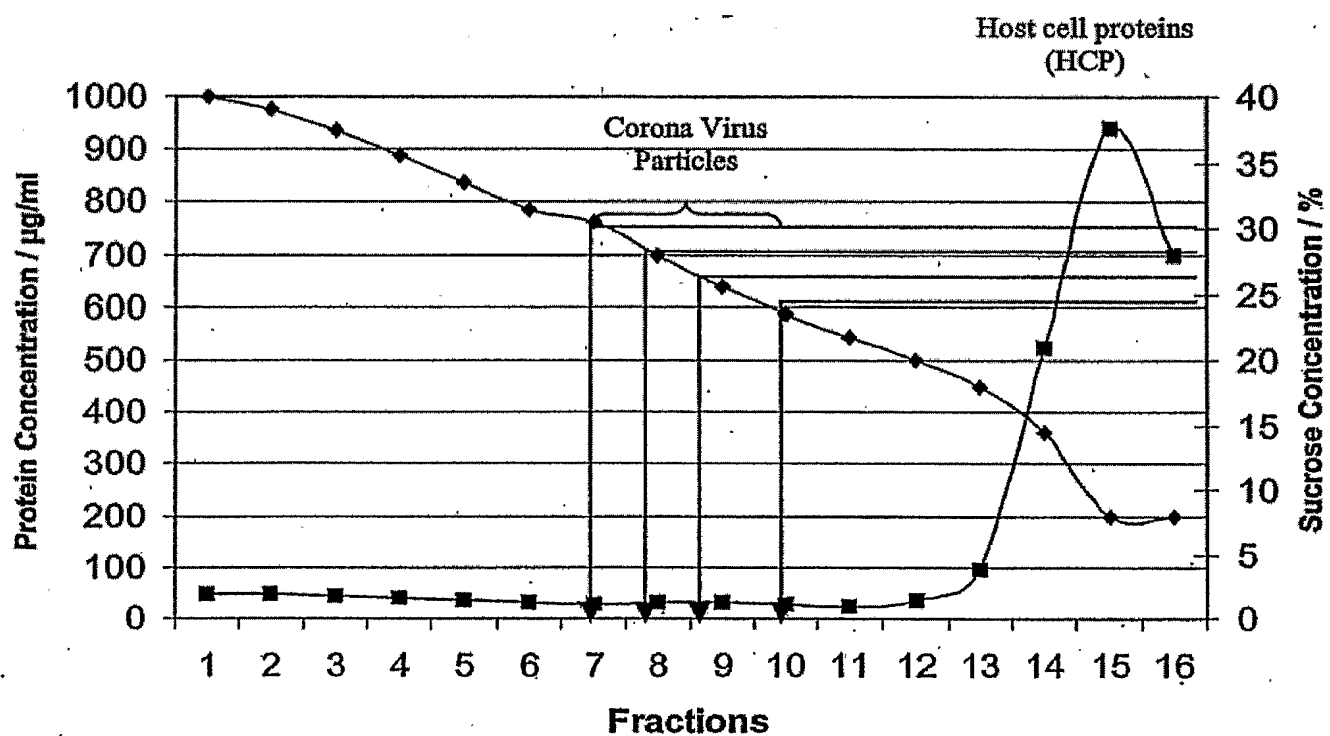
FIGURE 33**FIGURE 34**

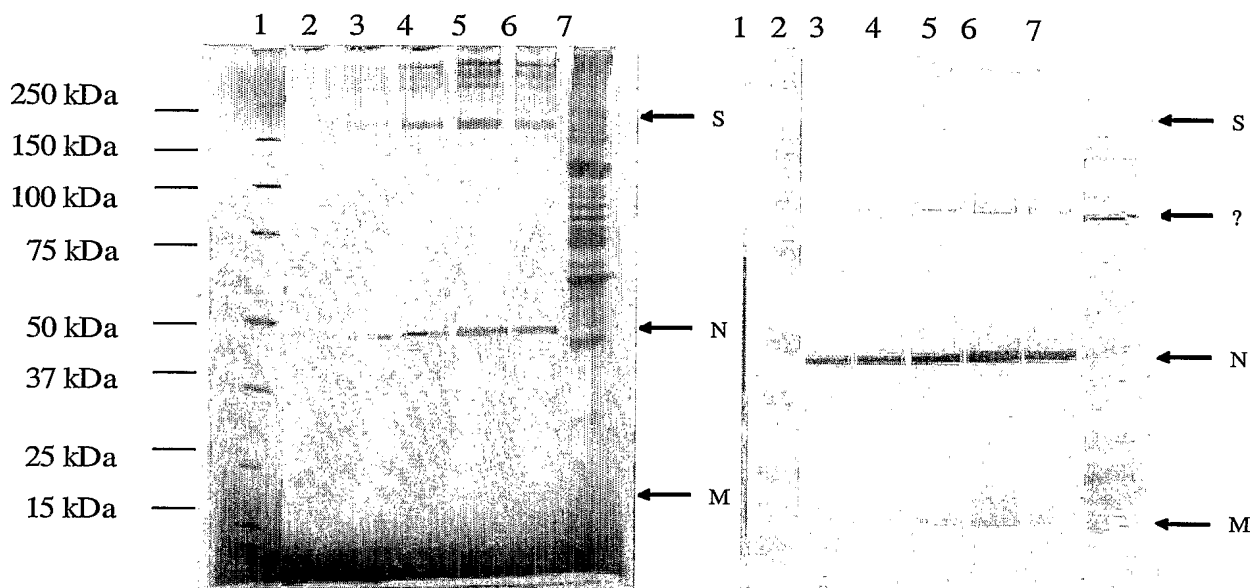
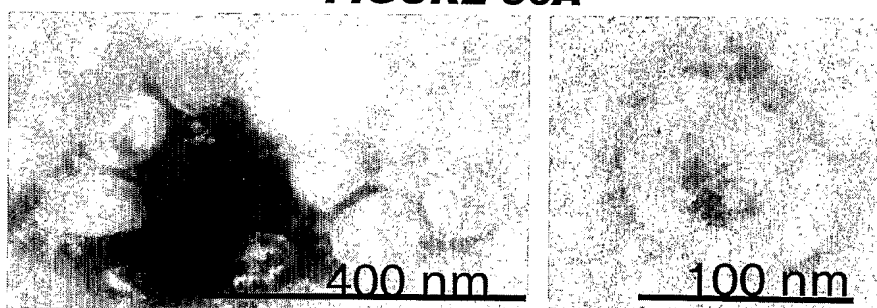
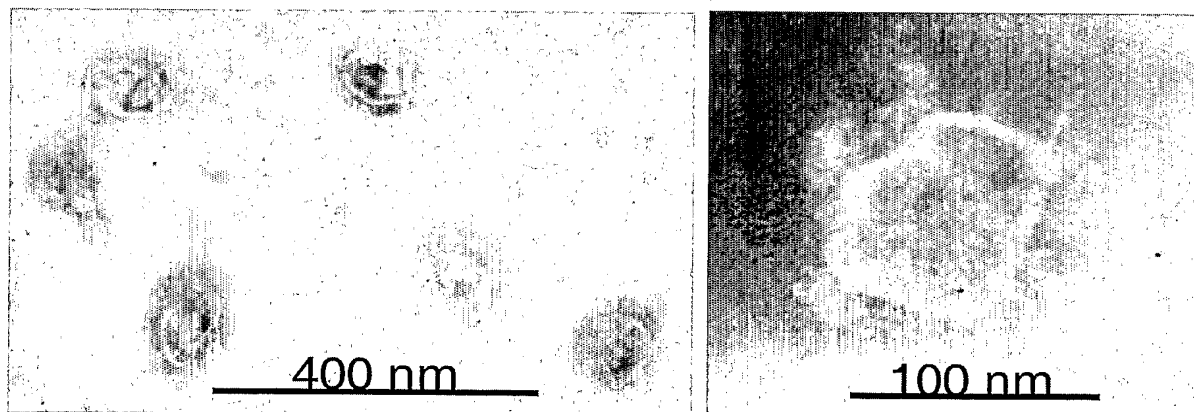
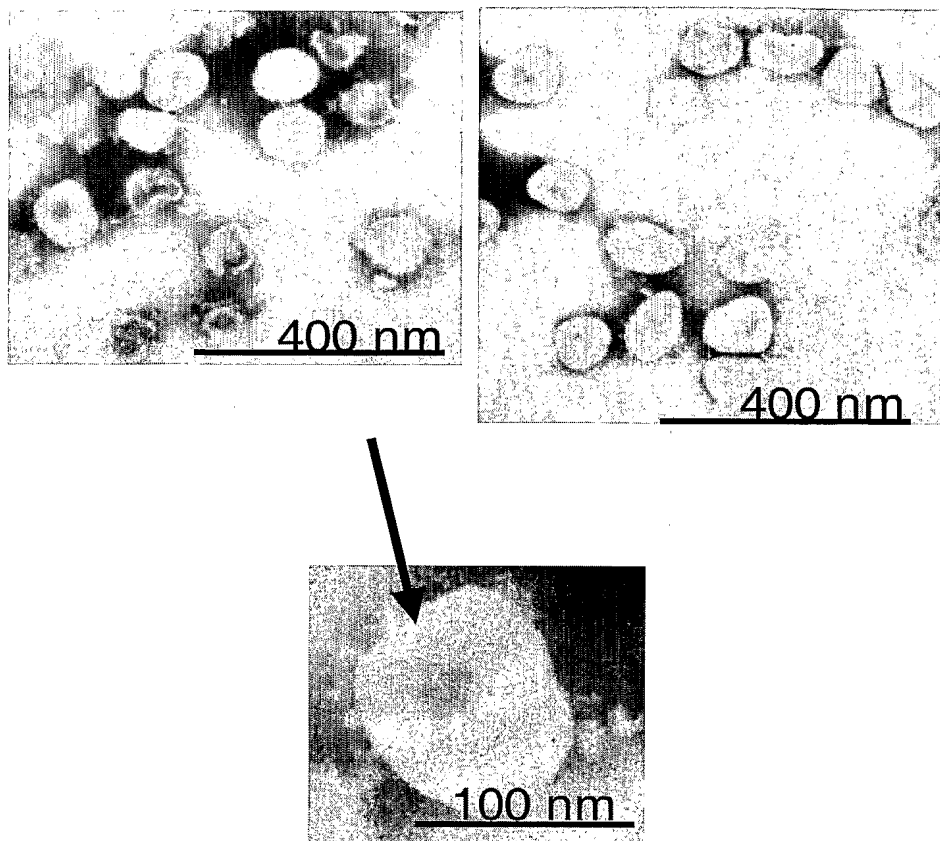
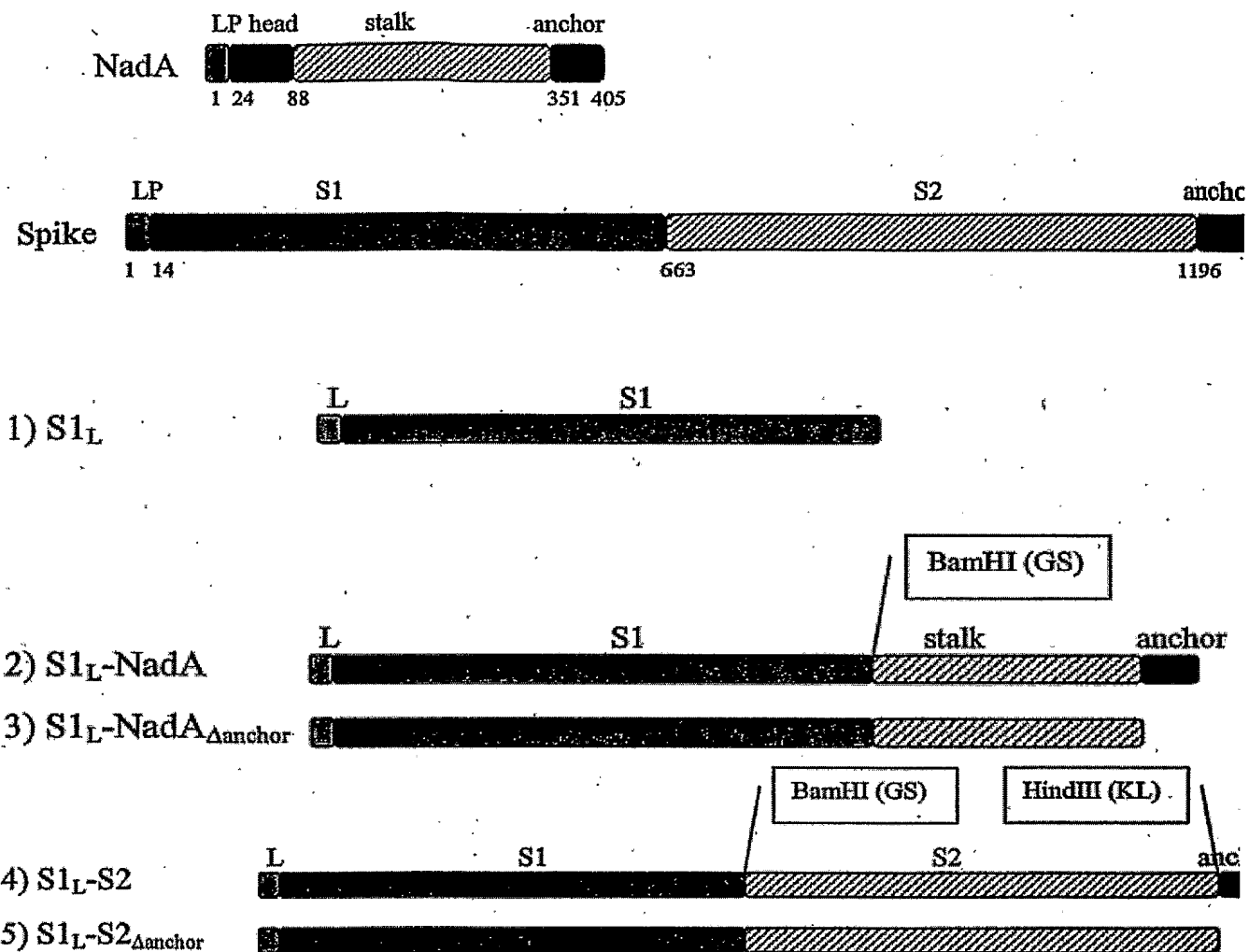
FIGURE 35**FIGURE 36****FIGURE 36A****FIGURE 36B**

FIGURE 36C

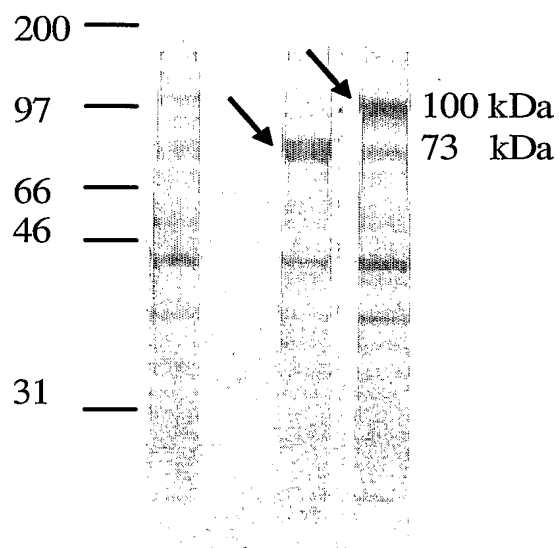
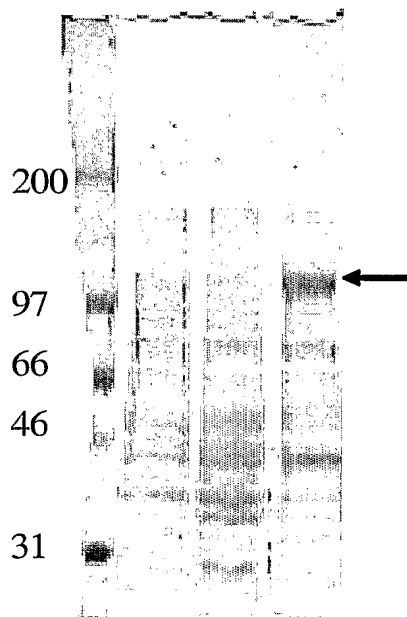
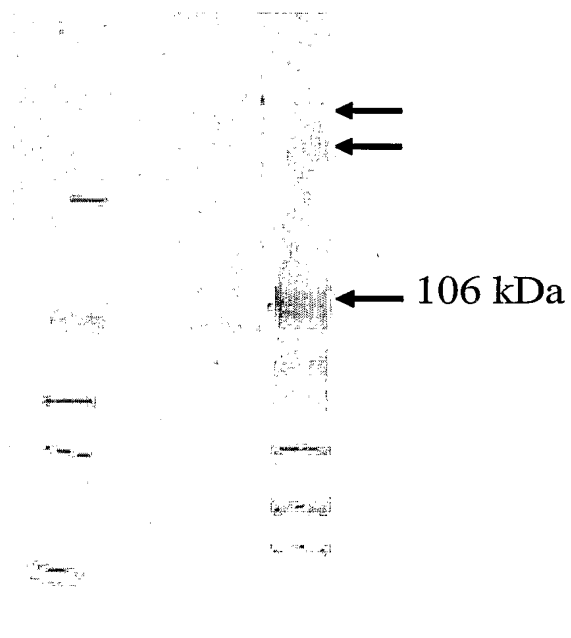


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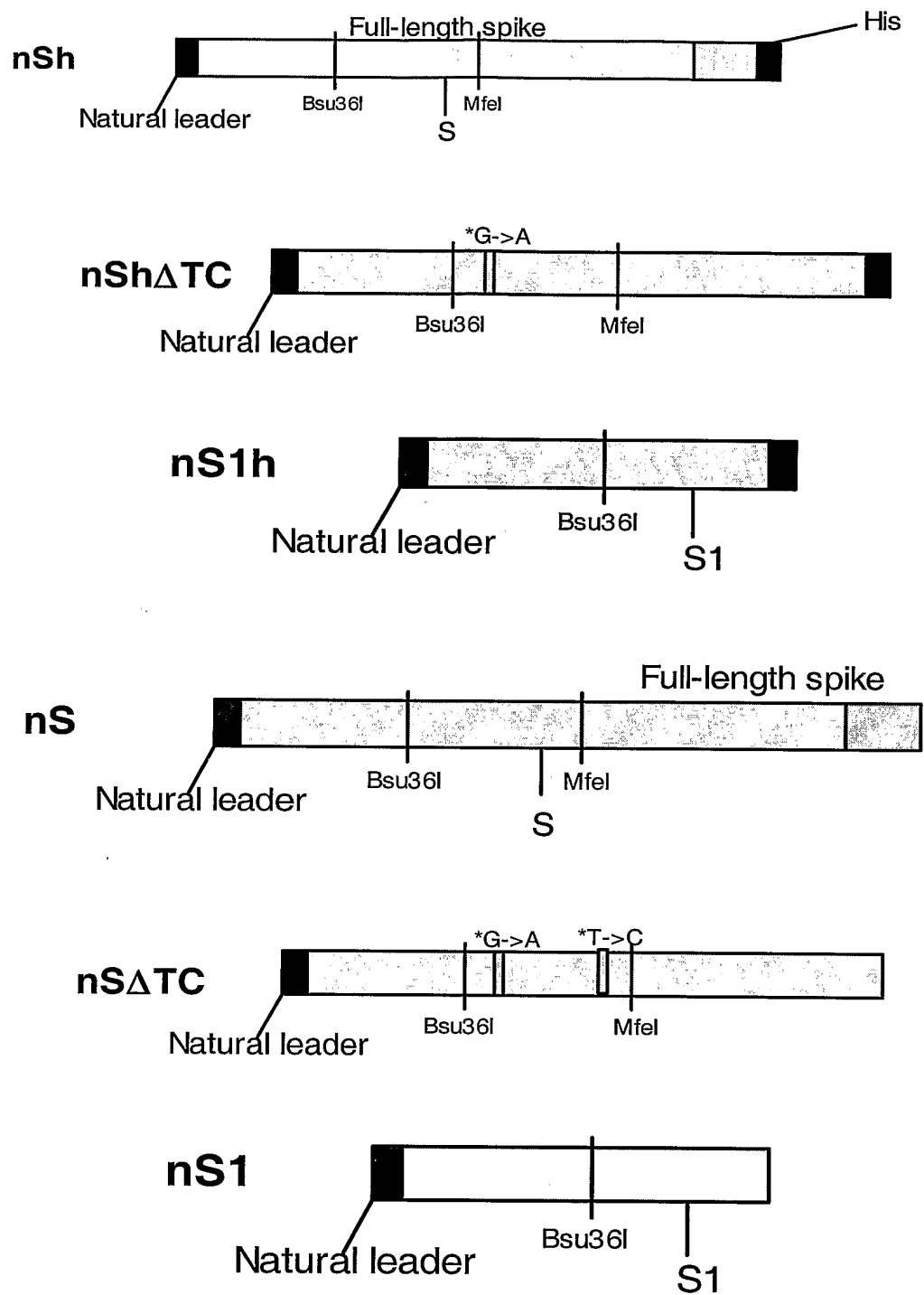
FIGURE 37



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FIGURE 38**FIGURE 39****FIGURE 39A****FIGURE 39B**

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FIGURE 40

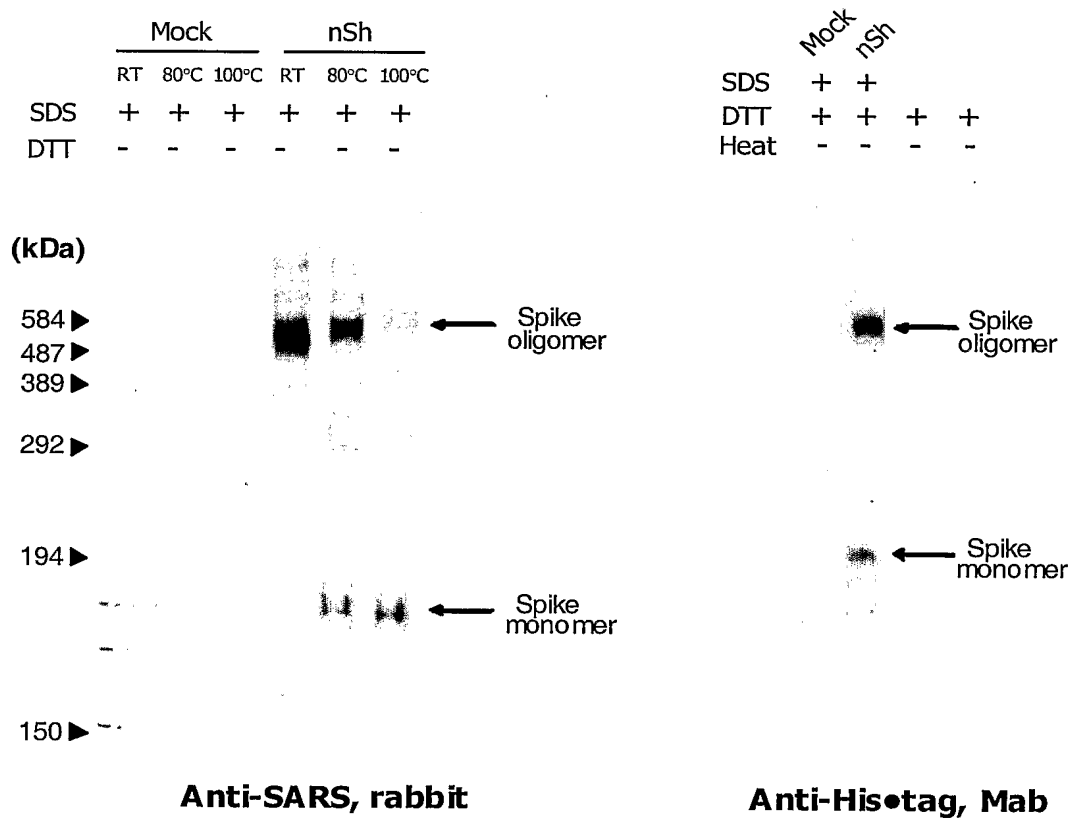


FIGURE 43

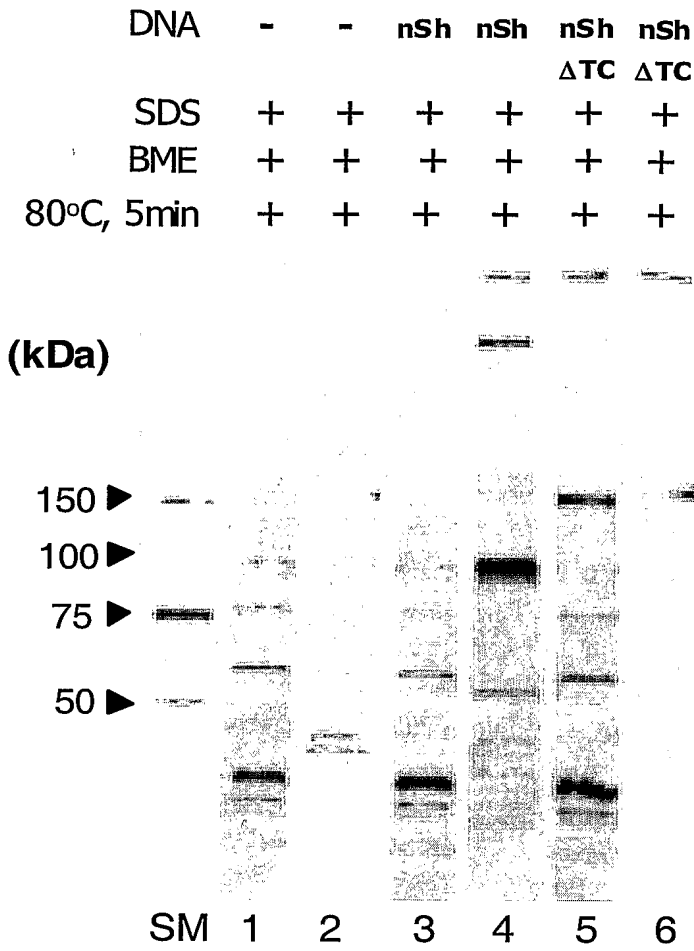


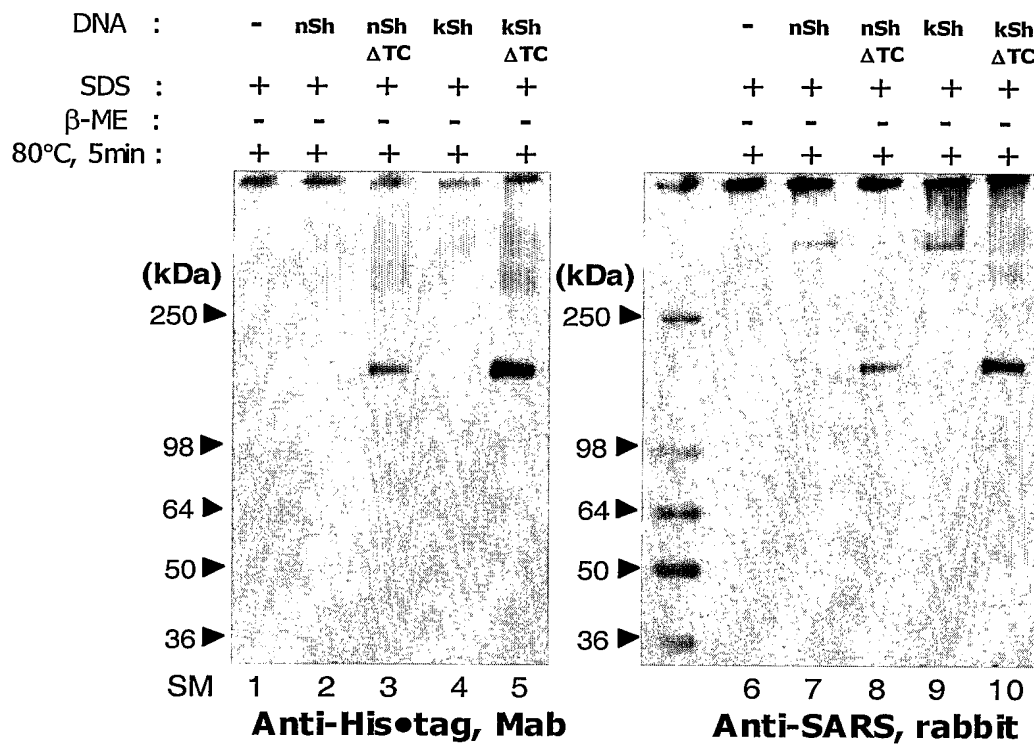
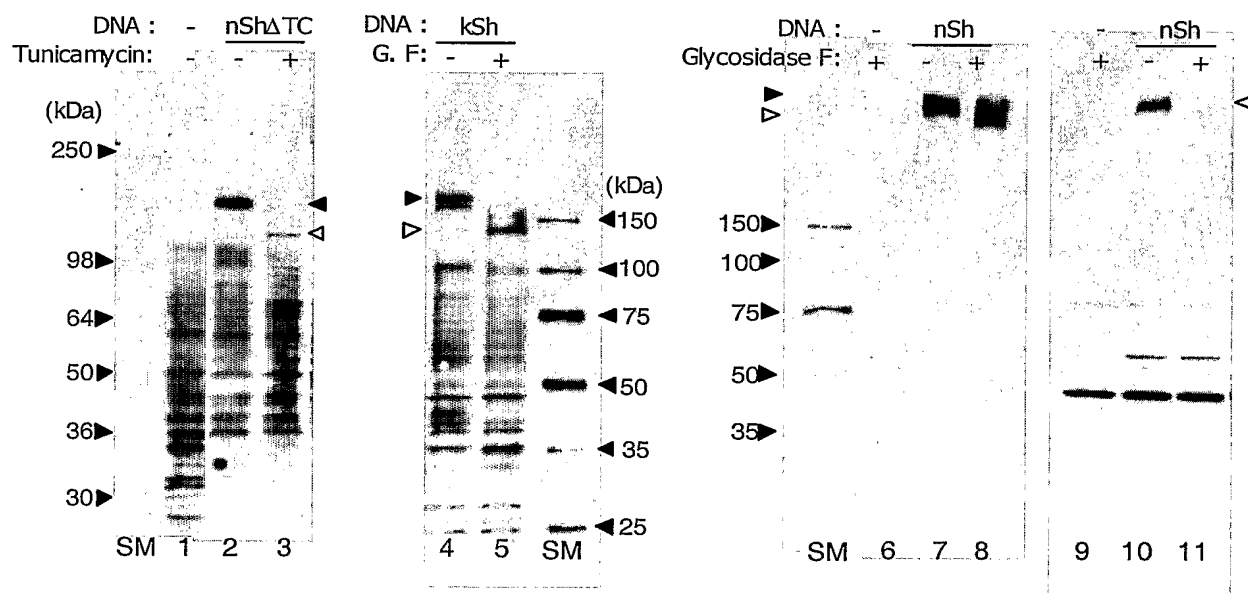
FIGURE 44**FIGURE 45**

FIGURE 46

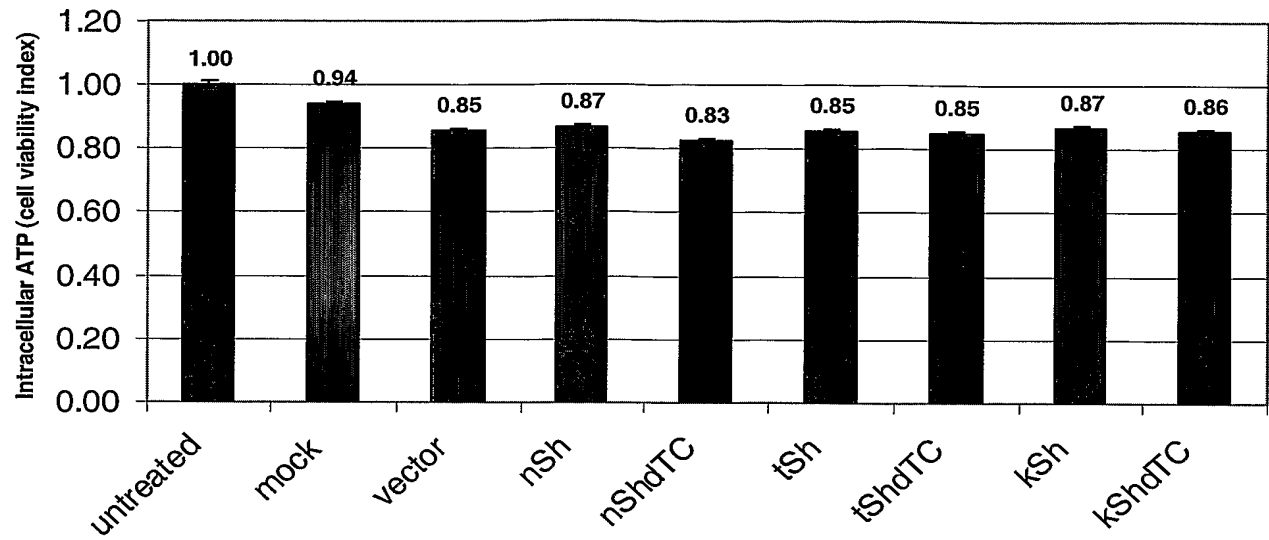
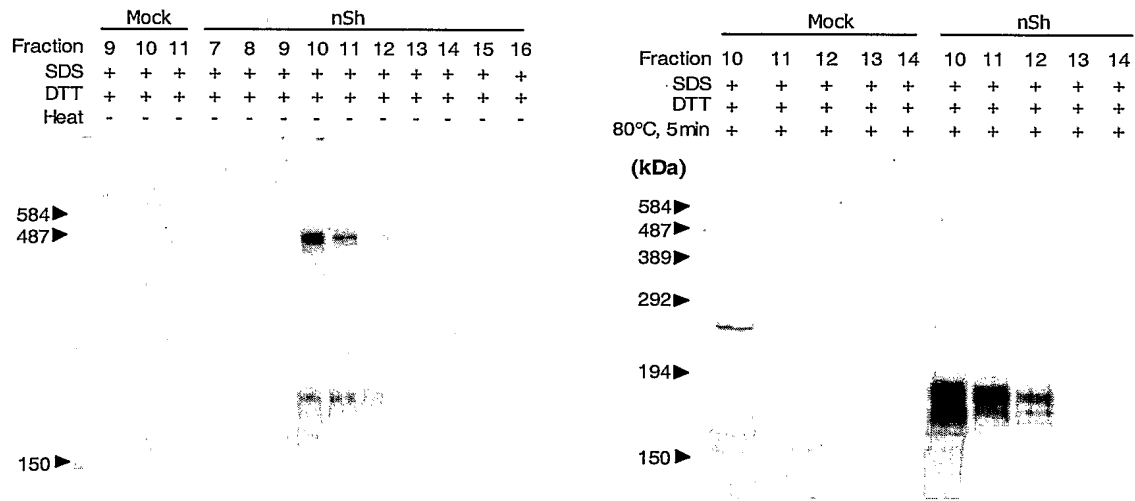
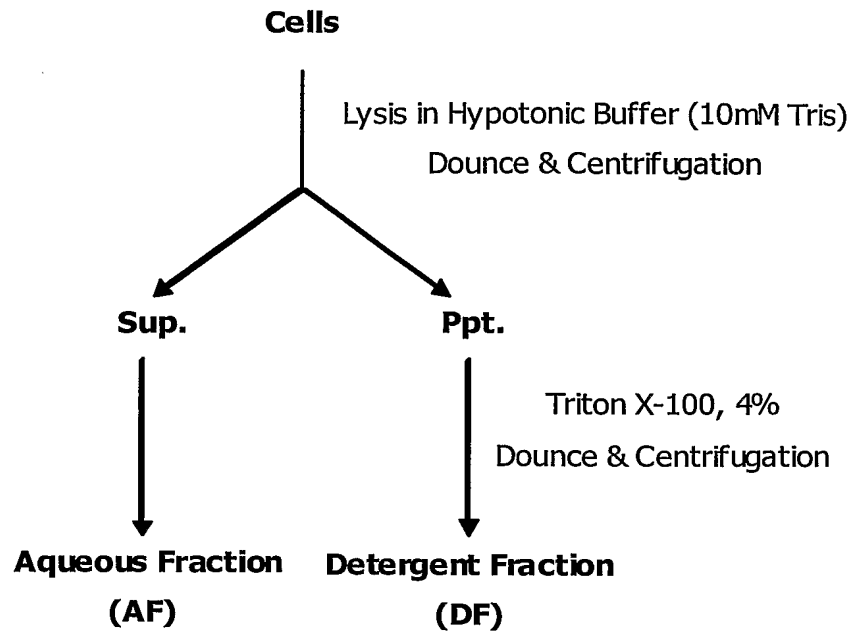
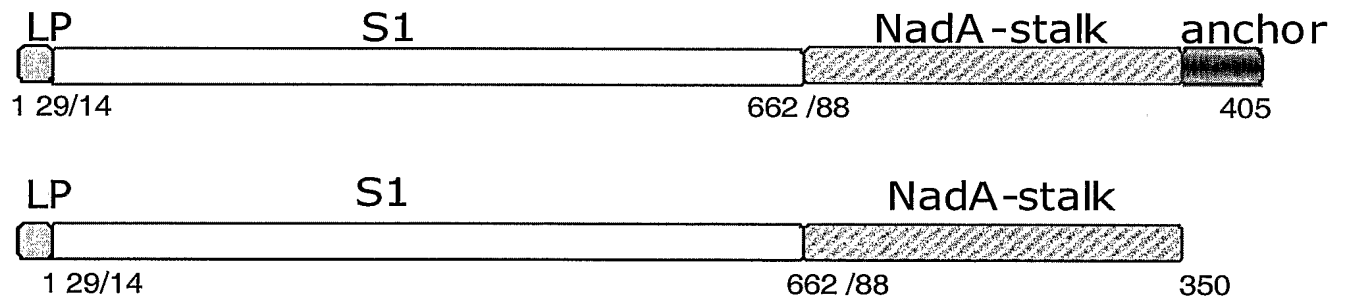


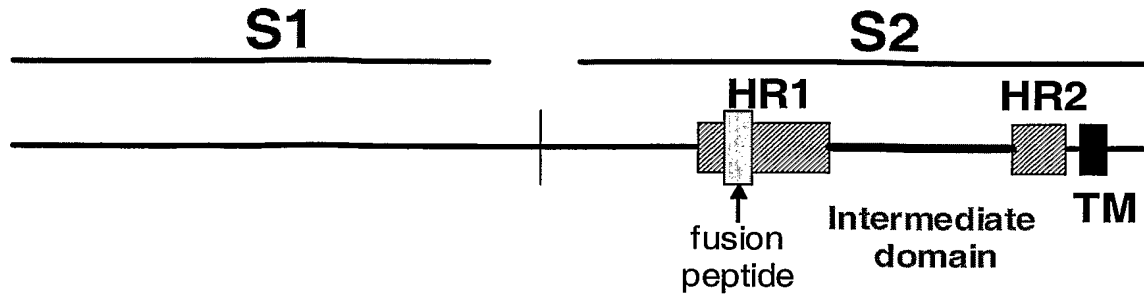
FIGURE 47



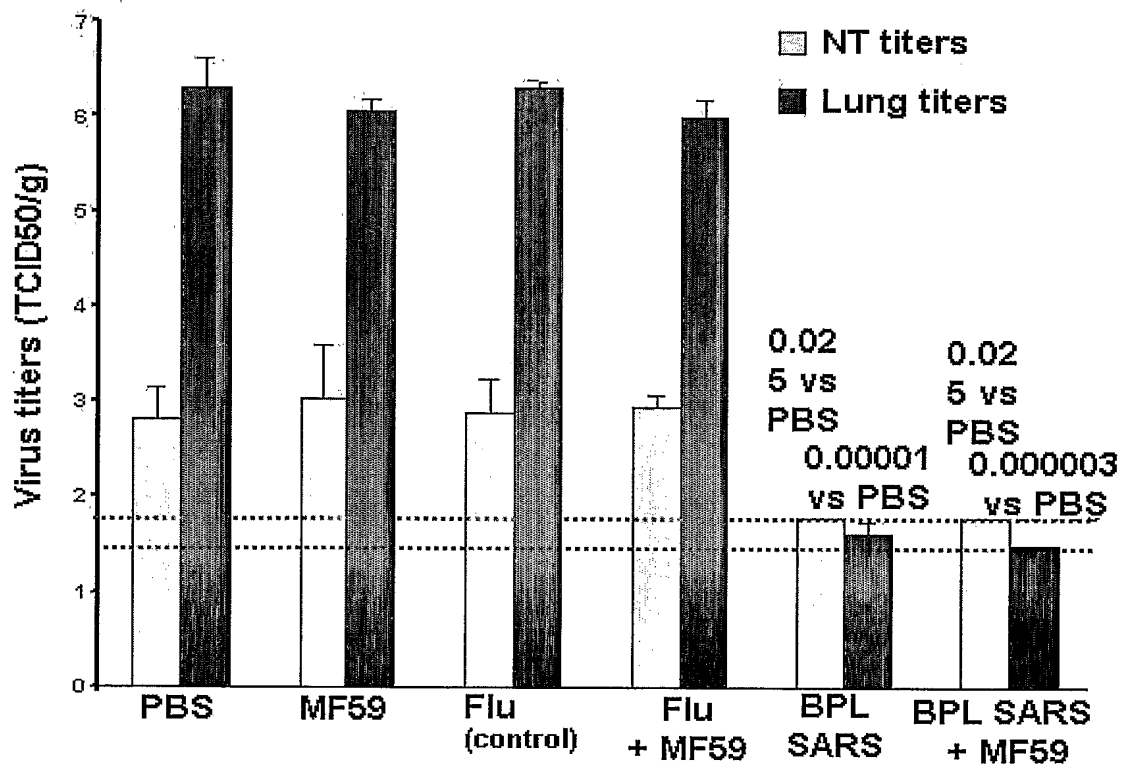
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FIGURE 48**FIGURE 49**

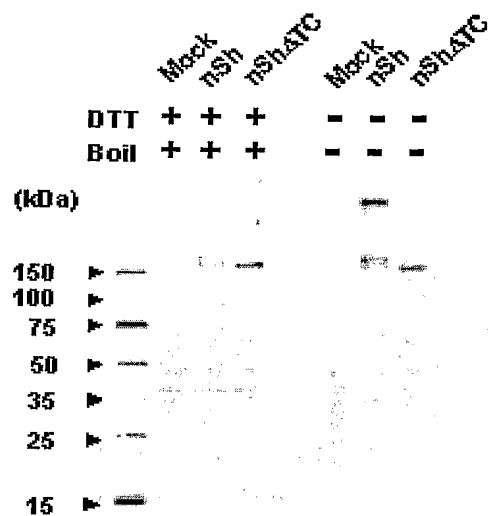
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FIGURE 50

- a) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- b) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)
- c) Leader(NadA)-HR1-intermediate-domain-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- d) Leader(NadA)-HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA)
- e) HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA) - HHHHHH
- f) Leader(NadA)-HR1-intermediate-domain-HR2-anchor(NadA)
- g) Leader(NadA)-HR1-intermediate-domain-HR2

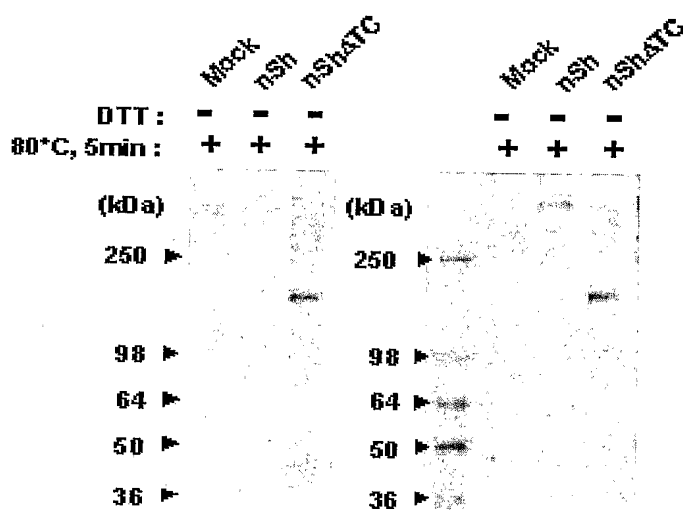
FIGURE 51

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FIGURE 52**A. 293 cell lysates**

Anti-His - tag, mAb

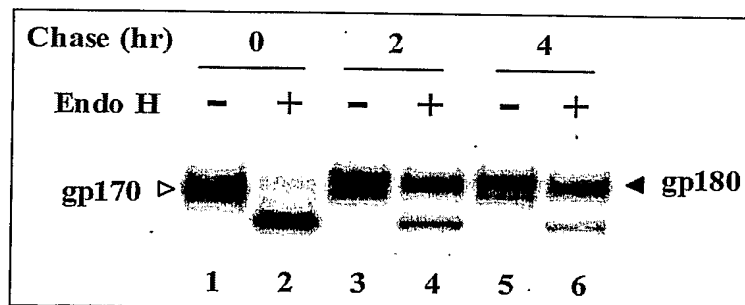
4-20% TG SDS gel

B. COS7 cell culture supernatants

Anti-His - tag, mAb

Anti-SARS, rabbit

4-20% TG SDS gel

FIGURE 53**FIGURE 55**

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FIGURE 54

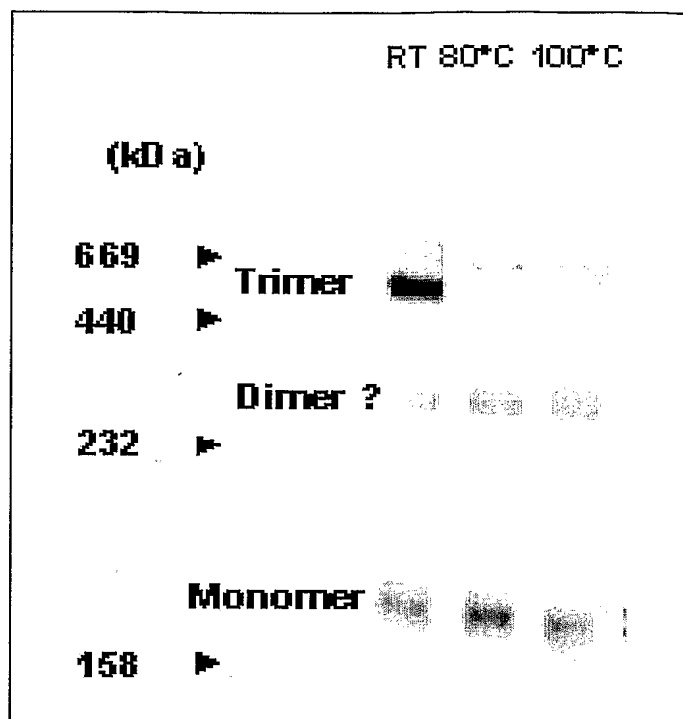


FIGURE 56

FIGURE 56A

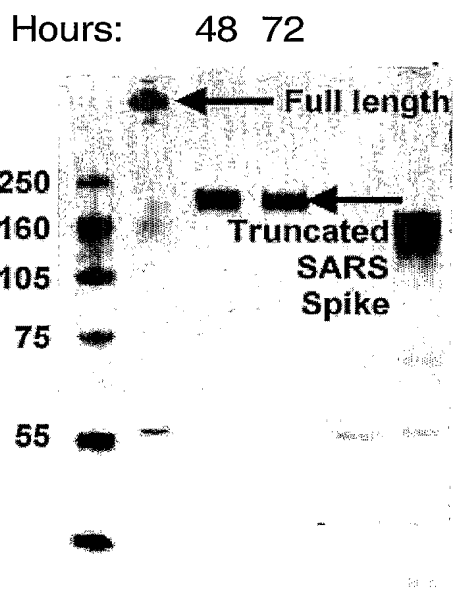


FIGURE 56B

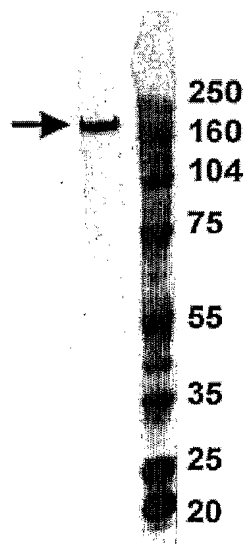
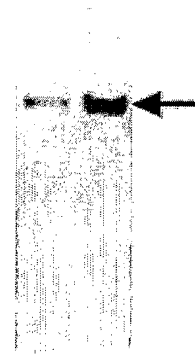
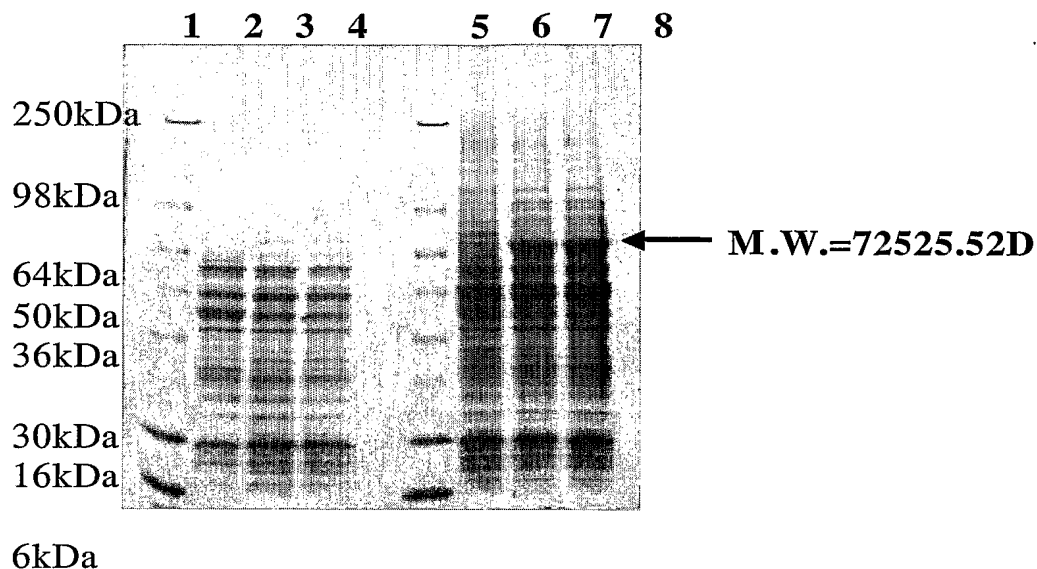
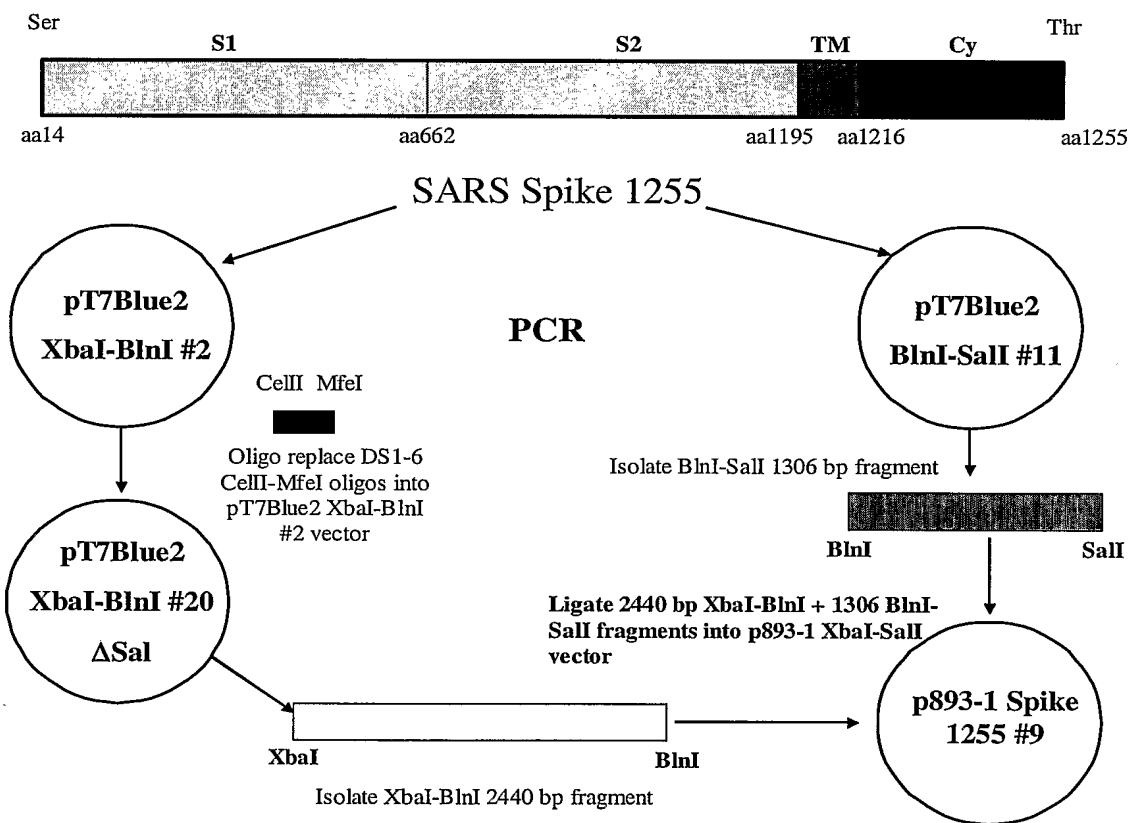


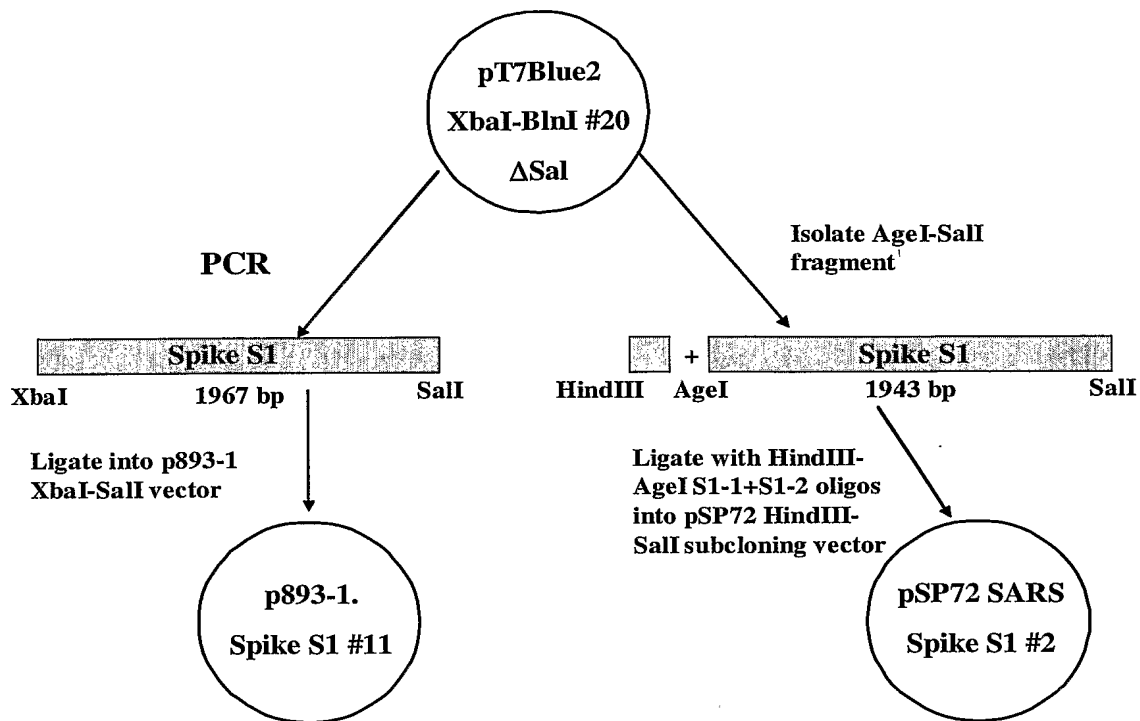
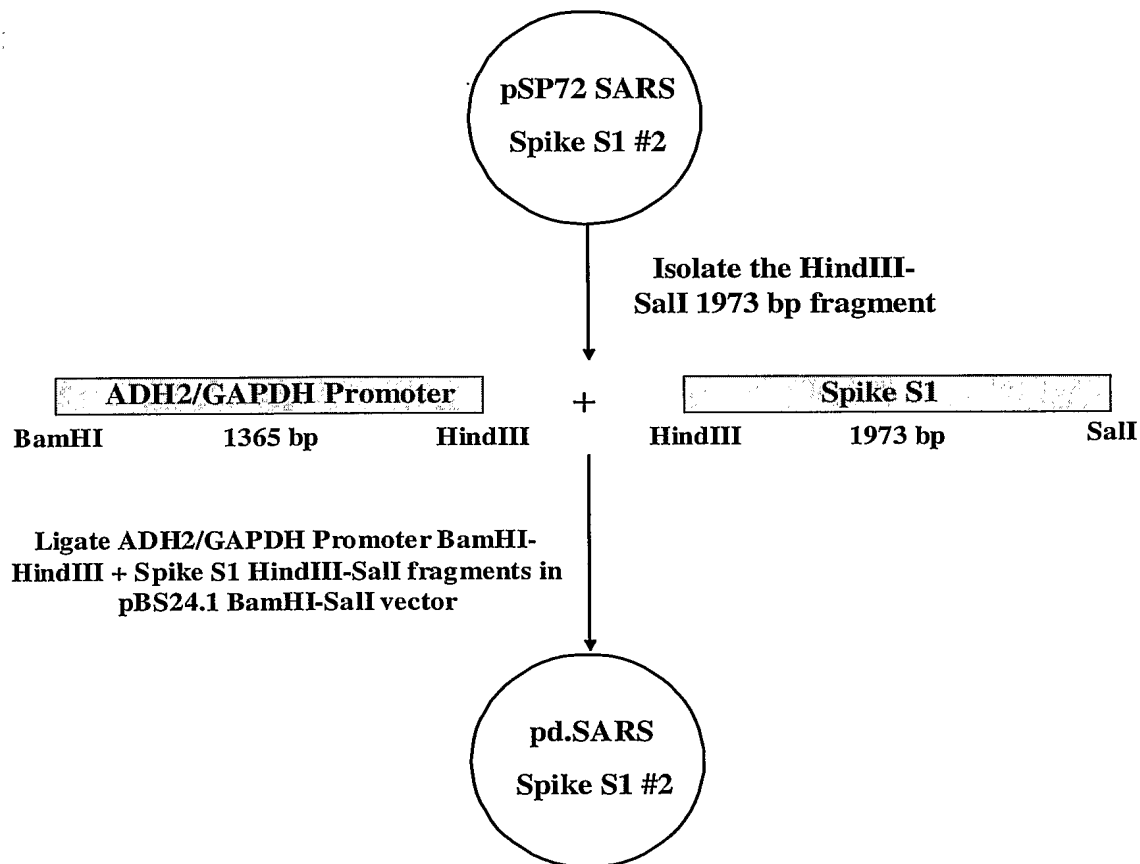
FIGURE 56C



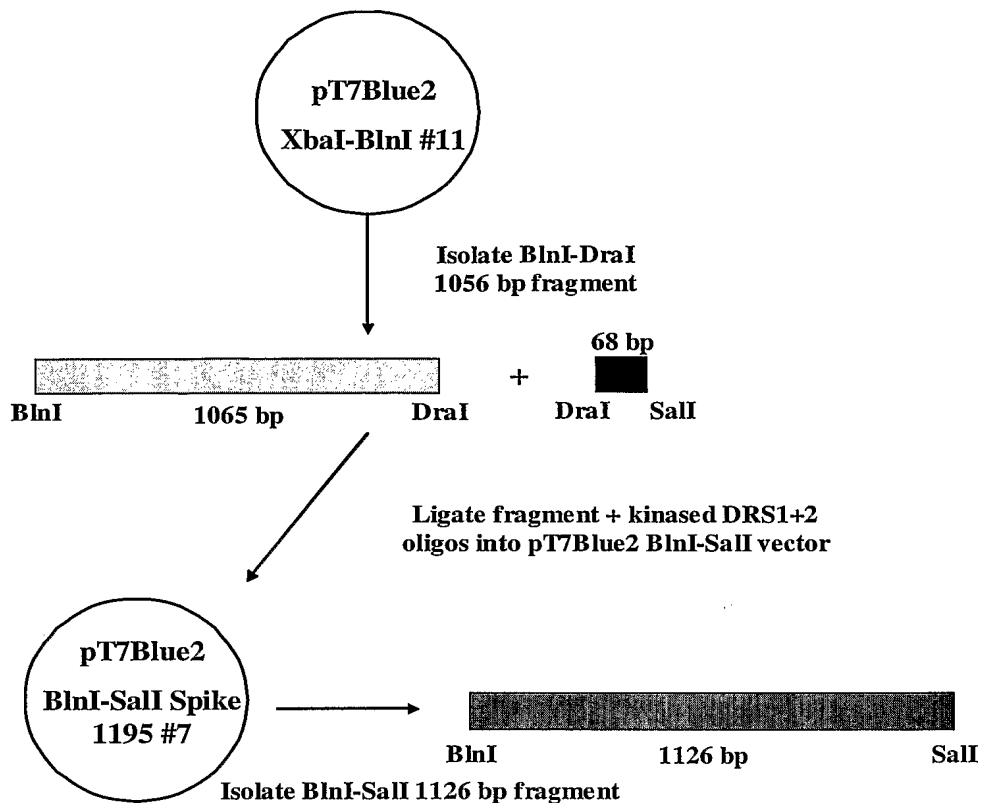
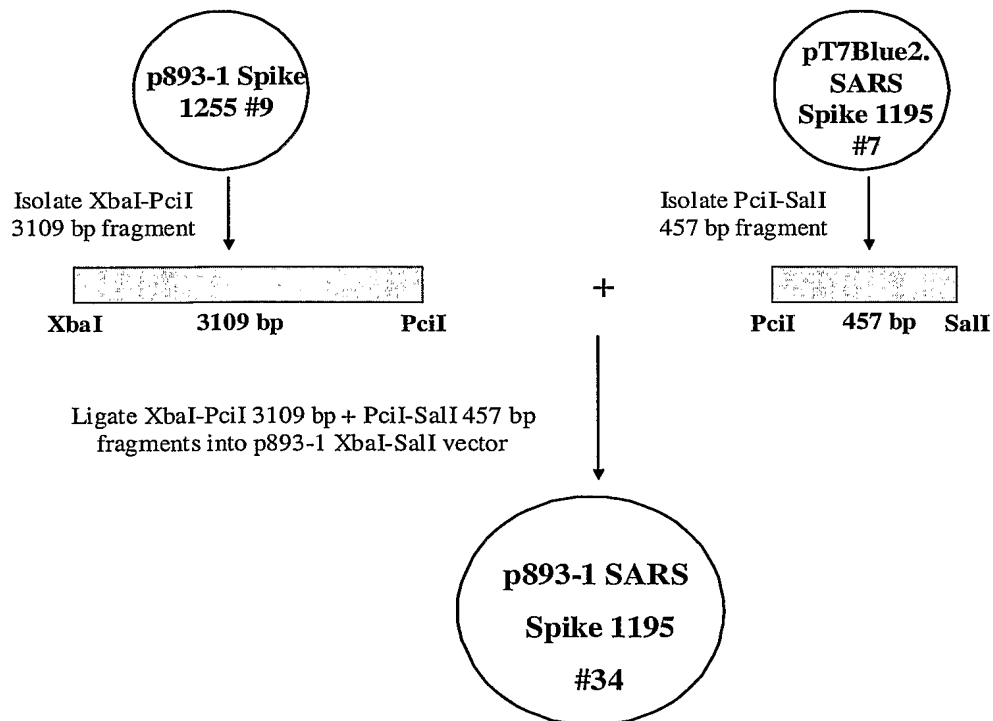
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FIGURE 57**FIGURE 58**

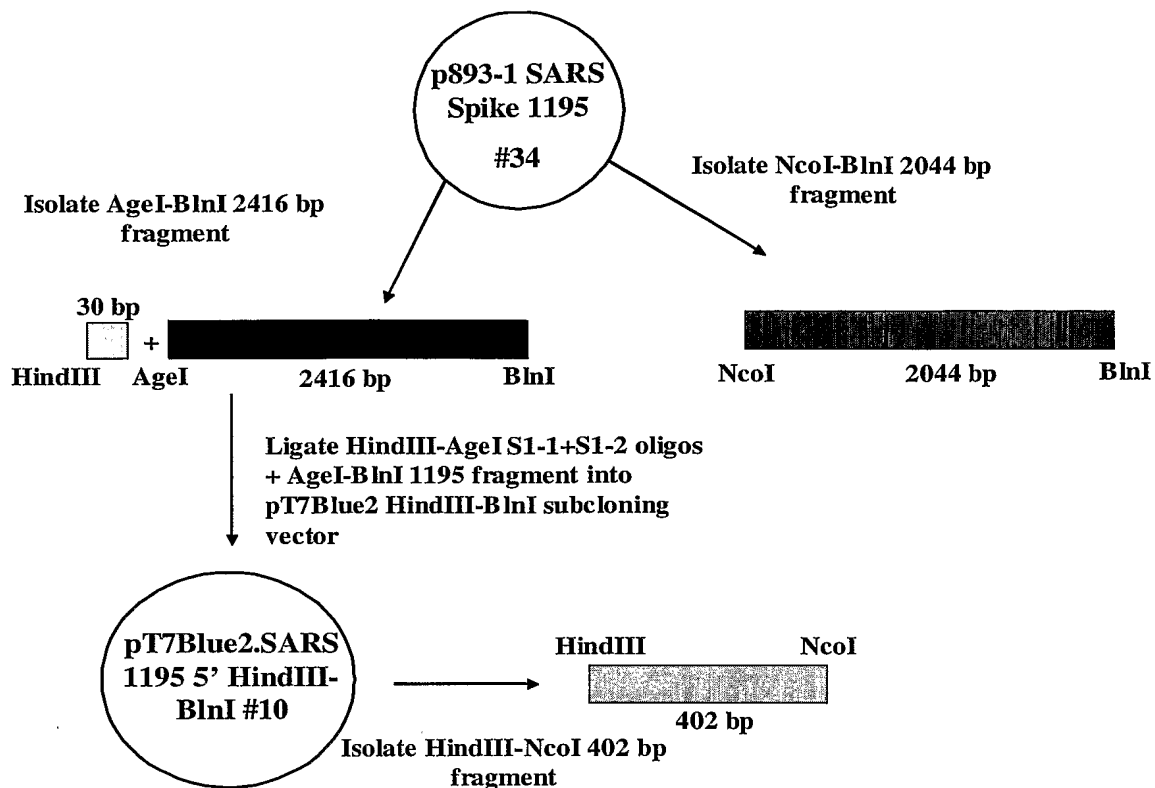
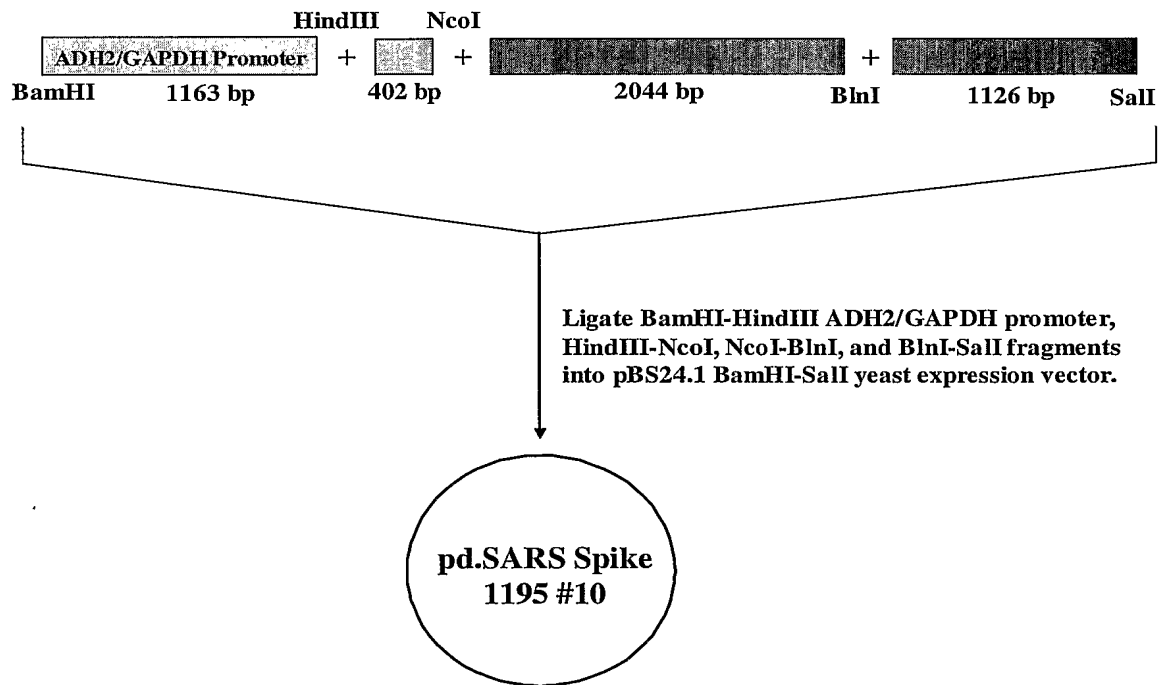
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FIGURE 59**FIGURE 60**

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FIGURE 61**FIGURE 62**

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FIGURE 63**FIGURE 64**

					1	M	S	D	L	D	R	C	T	T	F
AAGCTTACAAAACAAA					ATG	AGT	GAC	CTT	GAC	CGG	TGC	ACC	ACT	ACT	TTT
					20										
D	D	V	Q	A	P	N	Y	T	Q	H	T	S	S	M	
GAT	GAT	GTT	CAA	GCT	CCT	AAT	TAC	ACT	CAA	CAT	ACT	TCA	TCT	ATG	
					30										
R	G	V	Y	Y	P	D	E	I	F	R	S	D	T	L	
AGG	GGG	GTT	TAC	TAT	CCT	GAT	GAA	ATT	TTT	AGA	TCA	GAC	ACT	CTT	
					50										
Y	L	T	Q	D	L	F	L	P	F	Y	S	N	V	T	
TAT	TTA	ACT	CAG	GAT	TTA	TTT	CTT	CCA	TTT	TAT	TCT	AAT	GTT	ACA	
					60										
G	F	H	T	I	N	H	T	F	G	N	P	V	I	P	
GGG	TTT	CAT	ACT	ATT	AAT	CAT	ACG	TTT	GGC	AAC	CCT	GTC	ATA	CCT	
					80										
F	K	D	G	I	Y	F	A	A	T	E	K	S	N	V	
TTT	AAG	GAT	GGT	ATT	TAT	TTT	GCT	GCC	ACA	GAG	AAA	TCA	AAT	GTT	
					90										
V	R	G	W	V	F	G	S	T	M	N	N	K	S	Q	
GTC	CGT	GGT	TGG	GTT	TTT	GGT	TCT	ACC	ATG	AAC	AAC	AAG	TCA	CAG	
					110										
S	V	I	I	I	N	N	S	T	N	V	V	I	R	A	
TCG	GTG	ATT	ATT	ATT	AAC	AAT	TCT	ACT	AAT	GTT	GTT	ATA	CGA	GCA	
					120										
C	N	F	E	L	C	D	N	P	F	F	A	V	S	K	
TGT	AAC	TTT	GAA	TTG	TGT	GAC	AAC	CCT	TTC	TTT	GCT	GTT	TCT	AAA	
					140										
P	M	G	T	Q	T	H	T	M	I	F	D	N	A	F	
CCC	ATG	GGT	ACA	CAG	ACA	CAT	ACT	ATG	ATA	TTC	GAT	AAT	GCA	TTT	
					150										
N	C	T	F	E	Y	I	S	D	A	F	S	L	D	V	
AAT	TGC	ACT	TTC	GAG	TAC	ATA	TCT	GAT	GCC	TTT	TCG	CTT	GAT	GTT	
					170										
S	E	K	S	G	N	F	K	H	L	R	E	F	V	F	
TCA	GAA	AAG	TCA	GGT	AAT	TTT	AAA	CAC	TTA	CGA	GAG	TTT	GTG	TTT	
					180										
K	N	K	D	G	F	L	Y	V	Y	K	G	Y	Q	P	
AAA	AAT	AAA	GAT	GGG	TTT	CTC	TAT	GTT	TAT	AAG	GGC	TAT	CAA	CCT	

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200
 I D V V R D L P S G F N T L K
 ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA

210
 P I F K L P L G I N I T N F R
 CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA

230
 A I L T A F S P A Q D I W G T
 GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG

240
 S A A A Y F V G Y L K P T T F
 TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT

260
 M L K Y D E N G T I T D A V D
 ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT

270
 C S Q N P L A E L K C S V K S
 TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC

290
 F E I D K G I Y Q T S N F R V
 TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT

300
 V P S G D V V R F P N I T N L
 GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG

320
 C P F G E V F N A T K F P S V
 TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC

330
 Y A W E R K K I S N C V A D Y
 TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC

350
 S V L Y N S T F F S T F K C Y
 TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT

360
 G V S A T K L N D L C F S N V
 GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC

380
 Y A D S F V V K G D D V R Q I
 TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA

390
 A P G Q T G V I A D Y N Y K L
 GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

400

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410
 P D D F M G C V L A W N T R N
 CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC

420
 I D A T S T G N Y N Y K Y R Y
 ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT

430
 L R H G K L R P F E R D I S N
 CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT

440
 V P F S P D G K P C T P P A L
 GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT

450
 N C Y W P L N D Y G F Y T T T
 AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT

460
 G I G Y Q P Y R V V V L S F E
 GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA

470
 L L N A P A T V C G P K L S T
 CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT

480
 D L I K N Q C V N F N F N G L
 GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC

490
 T G T G V L T P S S K R F Q P
 ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA

500
 F Q Q F G R D V S D F T D S V
 TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT

510
 R D P K T S E I L D I S P C S
 CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT

520
 F G G V S V I T P G T N A S S
 TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT

530
 E V A V L Y Q D V N C T D V S
 GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT

540
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

550
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

560
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

570
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

580
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

590
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

600
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

610
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

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620

S T G N N V F Q T Q A G C L I
TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA

630

640

G A E H V D T S Y E C D I P I
GGA GCT GAG CAT GTT GAT ACT TCT TAT GAG TGC GAC ATT CCT ATT

650

G A G I C A S Y H T OC **SEQ ID NO: 9799**
GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA TAA TGAGTCGAC **SEQ ID NO: 9800**

Translated Mol. Weight = 72525.52

FIGURE 66

1

10

AAGCTTACAAAACAAA M S D L D R C T T F
ATG AGT GAC CTT GAC CGG TGC ACC ACT TTT

20

D D V Q A P N Y T Q H T S S M
GAT GAT GTT CAA GCT CCT AAT TAC ACT CAA CAT ACT TCA TCT ATG

30

40

R G V Y Y P D E I F R S D T L
AGG GGG GTT TAC TAT CCT GAT GAA ATT TTT AGA TCA GAC ACT CTT

50

Y L T Q D L F L P F Y S N V T
TAT TTA ACT CAG GAT TTA TTT CTT CCA TTT TAT TCT AAT GTT ACA

60

70

G F H T I N H T F G N P V I P
GGG TTT CAT ACT ATT AAT CAT ACG TTT GGC AAC CCT GTC ATA CCT

80

F K D G I Y F A A T E K S N V
TTT AAG GAT GGT ATT TAT TTT GCT GCC ACA GAG AAA TCA AAT GTT

90

100

V R G W V F G S T M N N K S Q
GTC CGT GGT TGG GTT TTT GGT TCT ACC ATG AAC AAC AAG TCA CAG

110

S V I I I N N S T N V V I R A
TCG GTG ATT ATT ATT AAC AAT TCT ACT AAT GTT GTT ATA CGA GCA

120

130

C N F E L C D N P F F A V S K
TGT AAC TTT GAA TTG TGT GAC AAC CCT TTC TTT GCT GTT TCT AAA

140

P M G T Q T H T M I F D N A F
CCC ATG GGT ACA CAG ACA CAT ACT ATG ATA TTC GAT AAT GCA TTT

150

160

N C T F E Y I S D A F S L D V
AAT TGC ACT TTC GAG TAC ATA TCT GAT GCC TTT TCG CTT GAT GTT

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170
 S E K S G N F K H L R E F V F
 TCA GAA AAG TCA GGT AAT TTT AAA CAC TTA CGA GAG TTT GTG TTT
 180
 K N K D G F L Y V Y K G Y Q P
 AAA AAT AAA GAT GGG TTT CTC TAT GTT TAT AAG GGC TAT CAA CCT
 190
 200
 I D V V R D L P S G F N T L K
 ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA
 210
 P I F K L P L G I N I T N F R
 CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA
 220
 230
 A I L T A F S P A Q D I W G T
 GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG
 240
 S A A A Y F V G Y L K P T T F
 TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT
 250
 260
 M L K Y D E N G T I T D A V D
 ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT
 270
 C S Q N P L A E L K C S V K S
 TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC
 280
 290
 F E I D K G I Y Q T S N F R V
 TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT
 300
 V P S G D V V R F P N I T N L
 GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG
 310
 320
 C P F G E V F N A T K F P S V
 TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC
 330
 Y A W E R K K I S N C V A D Y
 TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC
 340
 350
 S V L Y N S T F F S T F K C Y
 TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT
 360
 G V S A T K L N D L C F S N V
 GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC
 370
 380
 Y A D S F V V K G D D V R Q I
 TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA
 390
 A P G Q T G V I A D Y N Y K L
 GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG
 400

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410
 P D D F M G C V L A W N T R N
 CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC
 420 430
 I D A T S T G N Y N Y K Y R Y
 ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT
 440
 L R H G K L R P F E R D I S N
 CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT
 450 460
 V P F S P D G K P C T P P A L
 GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT
 470
 N C Y W P L N D Y G F Y T T T
 AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT
 480 490
 G I G Y Q P Y R V V V L S F E
 GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA
 500
 L L N A P A T V C G P K L S T
 CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT
 510 520
 D L I K N Q C V N F N F N G L
 GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC
 530
 T G T G V L T P S S K R F Q P
 ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA
 540 550
 F Q Q F G R D V S D F T D S V
 TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT
 560
 R D P K T S E I L D I S P C S
 CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT
 570 580
 F G G V S V I T P G T N A S S
 TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT
 590
 E V A V L Y Q D V N C T D V S
 GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT
 600 610
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT
 620
 S T G N N V F Q T Q A G C L I
 TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA
 630 640
 G A E H V D T S Y E C D I P I

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GGA GCT GAG CAT GTC GAC ACT TCT TAT GAG TGC GAC ATT CCT ATT
 650
 G A G I C A S Y H T V S L L R
 GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA GTT TCT TTA TTA CGT
 660 670
 S T S Q K S I V A Y T M S L G
 AGT ACT AGC CAA AAA TCT ATT GTG GCT TAT ACT ATG TCT TTA GGT
 680
 A D S S I A Y S N N T I A I P
 GCT GAT AGT TCA ATT GCT TAC TCT AAT AAC ACC ATT GCT ATA CCT
 690 700
 T N F S I S I T T E V M P V S
 ACT AAC TTT TCA ATT AGC ATT ACT ACA GAA GTA ATG CCT GTT TCT
 710
 M A K T S V D C N M Y I C G D
 ATG GCT AAA ACC TCC GTA GAT TGT AAT ATG TAC ATC TGC GGA GAT
 720 730
 S T E C A N L L L Q Y G S F C
 TCT ACT GAA TGT GCT AAT TTG CTT CTC CAA TAT GGT AGC TTT TGC
 740
 T Q L N R A L S G I A A E Q D
 ACA CAA CTA AAT CGT GCA CTC TCA GGT ATT GCT GCT GAA CAG GAT
 750 760
 R N T R E V F A Q V K Q M Y K
 CGC AAC ACA CGT GAA GTG TTC GCT CAA GTC AAA CAA ATG TAC AAA
 770
 T P T L K Y F G G F N F S Q I
 ACC CCA ACT TTG AAA TAT TTT GGT GGT TTT AAT TTT TCA CAA ATA
 780 790
 L P D P L K P T K R S F I E D
 TTA CCT GAC CCT CTA AAG CCA ACT AAG AGG TCT TTT ATT GAG GAC
 800
 L L F N K V T L A D A G F M K
 TTG CTC TTT AAT AAG GTG ACA CTC GCT GAT GCT GGC TTC ATG AAG
 810 820
 Q Y G E C L G D I N A R D L I
 CAA TAT GGC GAA TGC CTA GGT GAT ATT AAT GCT AGG GAC CTC ATT
 830
 C A Q K F N G L T V L P P L L
 TGT GCG CAG AAG TTC AAT GGA CTT ACA GTG TTG CCA CCT CTG CTC
 840 850
 T D D M I A A Y T A A L V S G
 ACT GAT GAT ATG ATT GCT GCC TAC ACT GCT GCT CTA GTT AGT GGT
 860
 T A T A G W T F G A G A A L Q
 ACT GCC ACT GCT GGA TGG ACA TTT GGT GCT GGC GCT GCT CTT CAA
 870 880

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I P F A M Q M A Y R F N G I G
 ATA CCT TTT GCT ATG CAA ATG GCA TAT AGG TTC AAT GGC ATT GGA
 890
 V T Q N V L Y E N Q K Q I A N
 GTT ACC CAA AAT GTT CTC TAT GAG AAC CAA AAA CAA ATC GCC AAC
 900 910
 Q F N K A I S Q I Q E S L T T
 CAA TTT AAC AAG GCG ATT AGT CAA ATT CAA GAA TCA CTT ACA ACA
 920
 T S T A L G K L Q D V V N Q N
 ACA TCA ACT GCA TTG GGC AAG CTG CAA GAC GTT GTT AAC CAG AAT
 930 940
 A Q A L N T L V K Q L S S N F
 GCT CAA GCA TTA AAC ACA CTT GTT AAA CAA CTT AGC TCT AAT TTT
 950
 G A I S S V L N D I L S R L D
 GGT GCA ATT TCA AGT GTG CTA AAT GAT ATC CTT TCG CGA CTT GAT
 960 970
 K V E A E V Q I D R L I T G R
 AAA GTC GAG GCG GAG GTA CAA ATT GAC AGG TTA ATT ACA GGC AGA
 980
 L Q S L Q T Y V T Q Q L I R A
 CTT CAA AGC CTT CAA ACC TAT GTA ACA CAA CAA CTA ATC AGG GCT
 990 1000
 A E I R A S A N L A A T K M S
 GCT GAA ATC AGG GCT TCT GCT AAT CTT GCT GCT ACT AAA ATG TCT
 1010
 E C V L G Q S K R V D F C G K
 GAG TGT GTT CTT GGA CAA TCA AAA AGA GTT GAC TTT TGT GGA AAG
 1020 1030
 G Y H L M S F P Q A A P H G V
 GGC TAC CAC CTT ATG TCC TTC CCA CAA GCA GCC CCG CAT GGT GTT
 1040
 V F L H V T Y V P S Q E R N F
 GTC TTC CTA CAT GTC ACG TAT GTG CCA TCC CAG GAG AGG AAC TTC
 1050 1060
 T T A P A I C H E G K A Y F P
 ACC ACA GCG CCA GCA ATT TGT CAT GAA GGC AAA GCA TAC TTC CCT
 1070
 R E G V F V F N G T S W F I T
 CGT GAA GGT GTT TTT GTG TTT AAT GGC ACT TCT TGG TTT ATT ACA
 1080 1090
 Q R N F F S P Q I I T T D N T
 CAG AGG AAC TTC TTT TCT CCA CAA ATA ATT ACT ACA GAC AAT ACA
 1100
 F V S G N C D V V I G I I N N
 TTT GTC TCA GGA AAT TGT GAT GTC GTT ATT GGC ATC ATT AAC AAC

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```

      1110
T   V   Y   D   P   L   Q   P   E   L   D   S   F   K   E
ACA GTT TAT GAT CCT CTG CAA CCT GAG CTT GAC TCA TTC AAA GAA

      1130
E   L   D   K   Y   F   K   N   H   T   S   P   D   V   D
GAG CTG GAC AAG TAC TTC AAA AAT CAT ACA TCA CCA GAT GTT GAT

      1140
F   G   D   I   S   G   I   N   A   S   V   V   N   I   Q
TTT GGC GAC ATT TCA GGC ATT AAC GCT TCT GTC GTC AAC ATT CAA

      1160
K   E   I   D   R   L   N   E   V   A   K   N   L   N   E
AAA GAA ATT GAC CGC CTC AAT GAG GTC GCT AAA AAT TTA AAT GAA

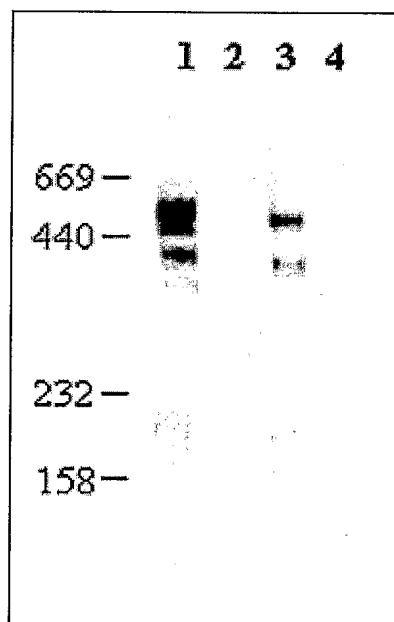
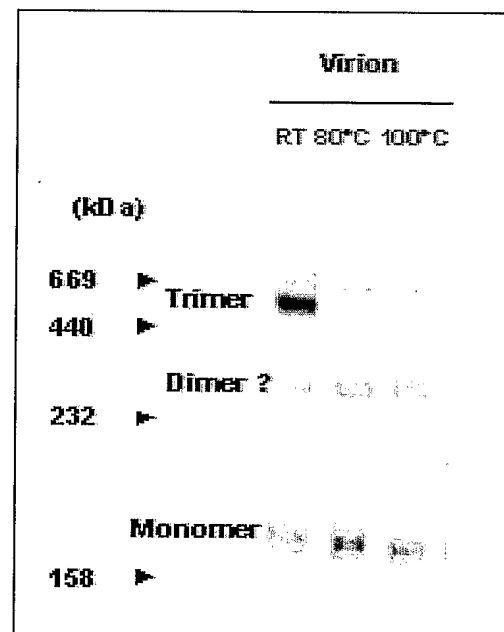
      1170
S   L   I   D   L   Q   E   L   G   K   Y   E   Q   Y   I
TCA CTC ATT GAC CTT CAA GAA TTG GGA AAA TAT GAG CAA TAT ATT

      1183
K   W   P   OC
AAA TGG CCT TAA TGAGTCGAC

```

Translated Mol. Weight = 131315.20

SEQ ID NO: 9801
SEQ ID NO: 9802

FIGURE 67**FIGURE 67A****FIGURE 67B**

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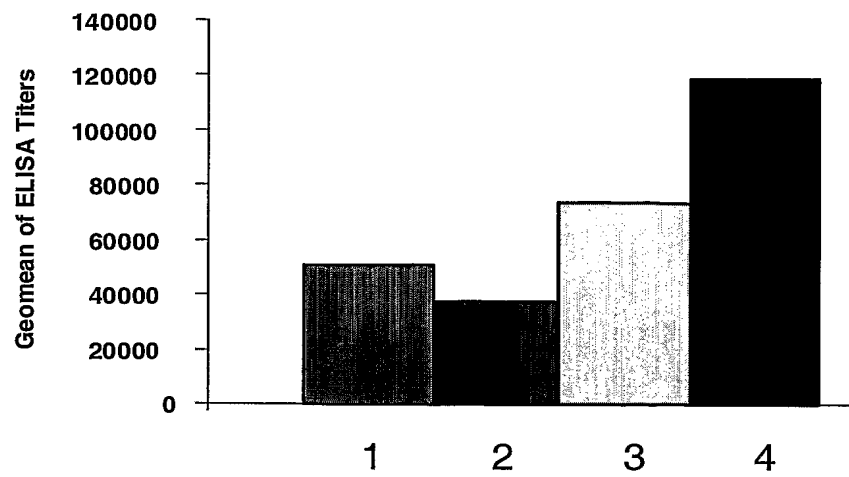
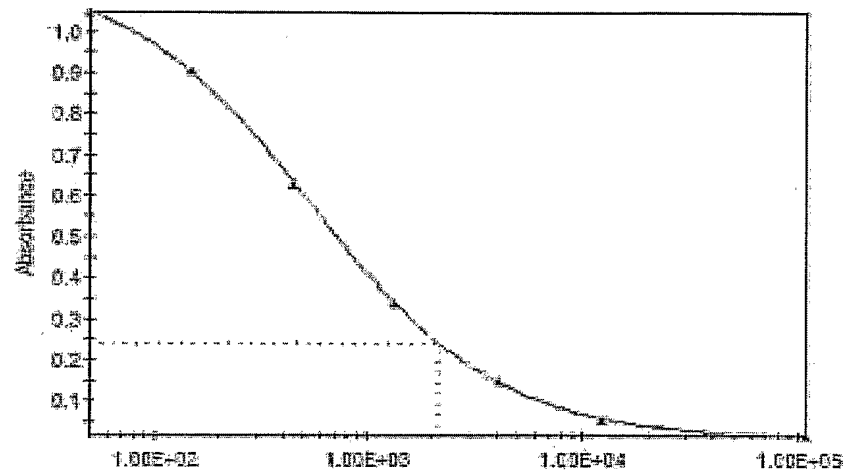
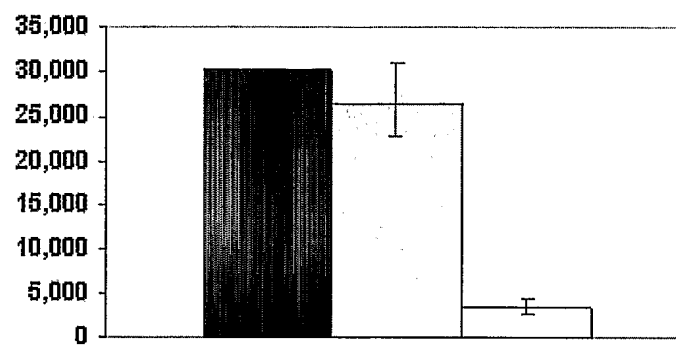
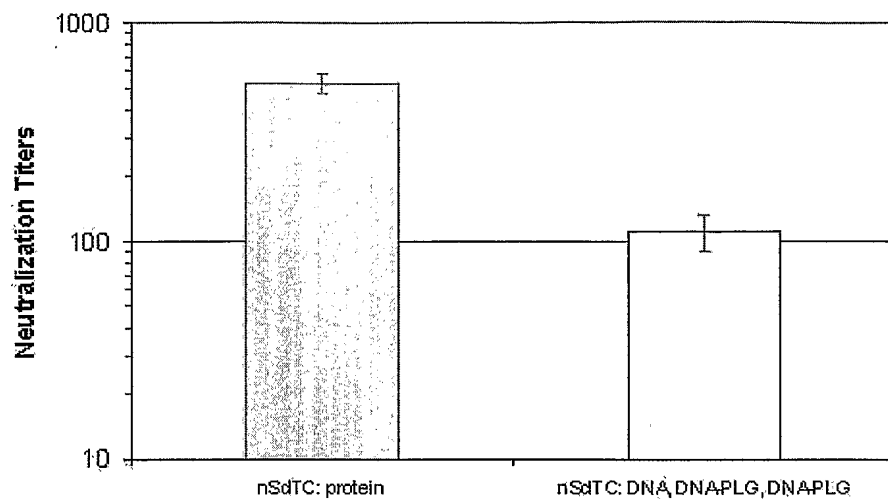
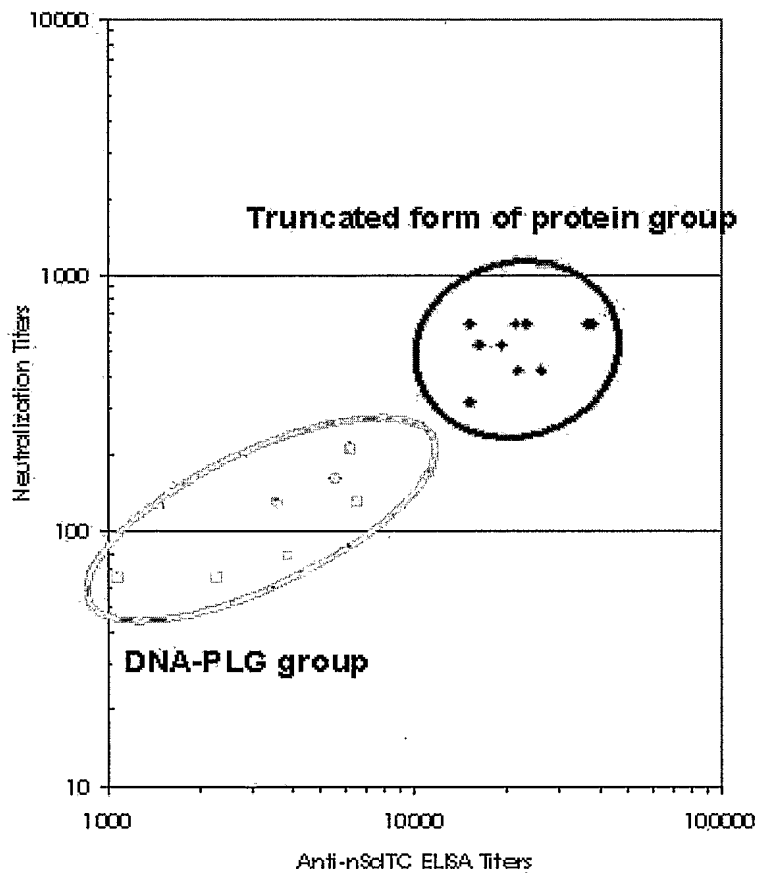
FIGURE 68**FIGURE 69****FIGURE 70**

FIGURE 71**FIGURE 72**

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FIGURE 73

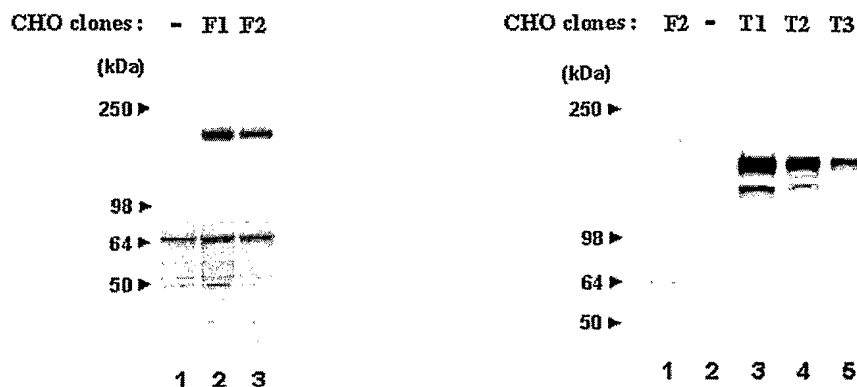


FIGURE 74

FIGURE 74A

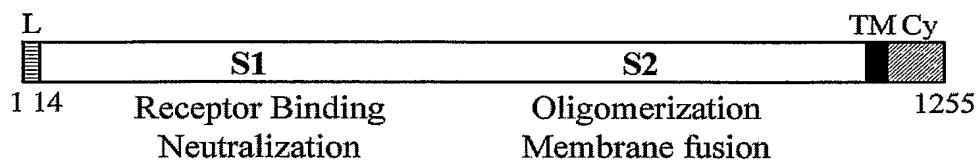


FIGURE 74B

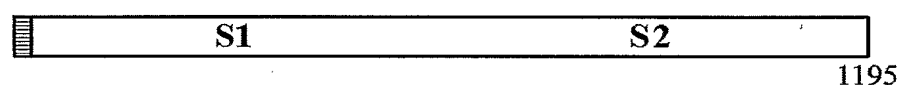


FIGURE 75

FIGURE 75A

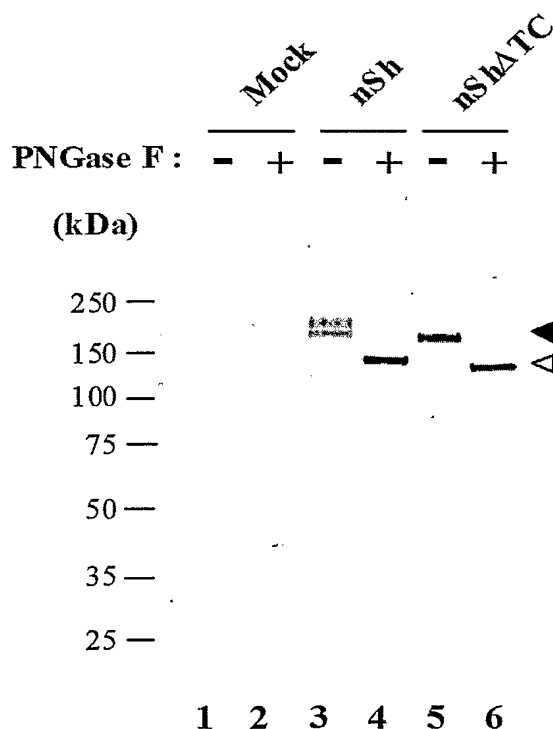


FIGURE 75B

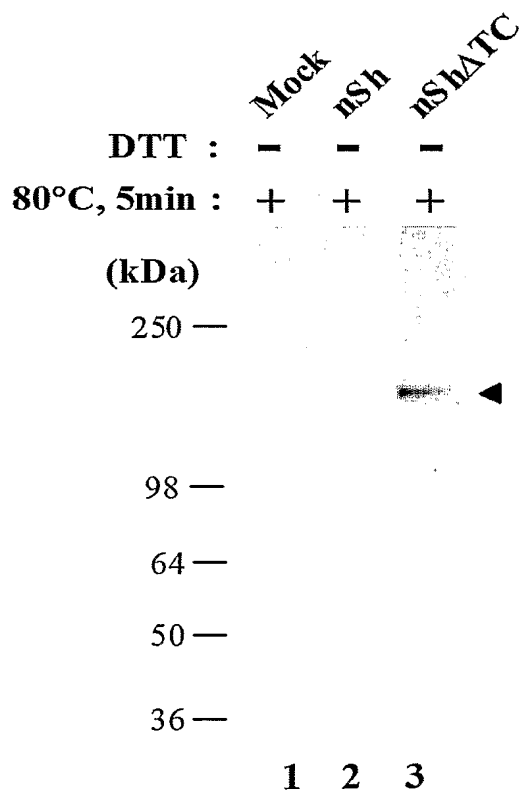
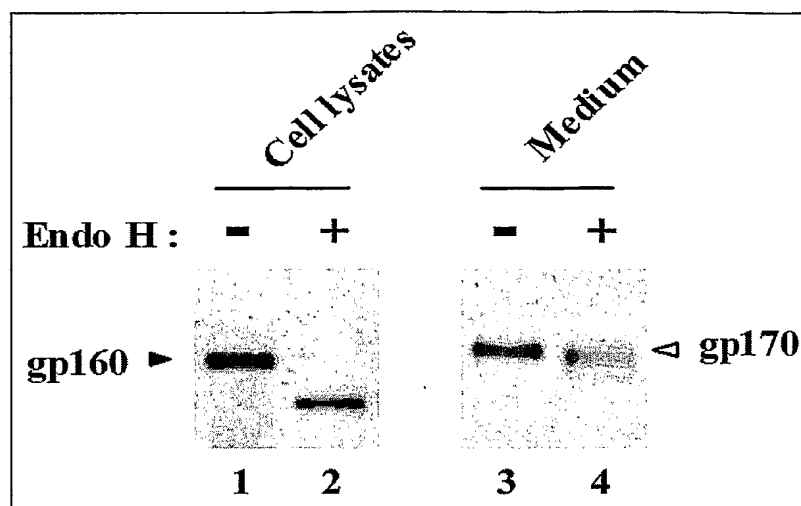
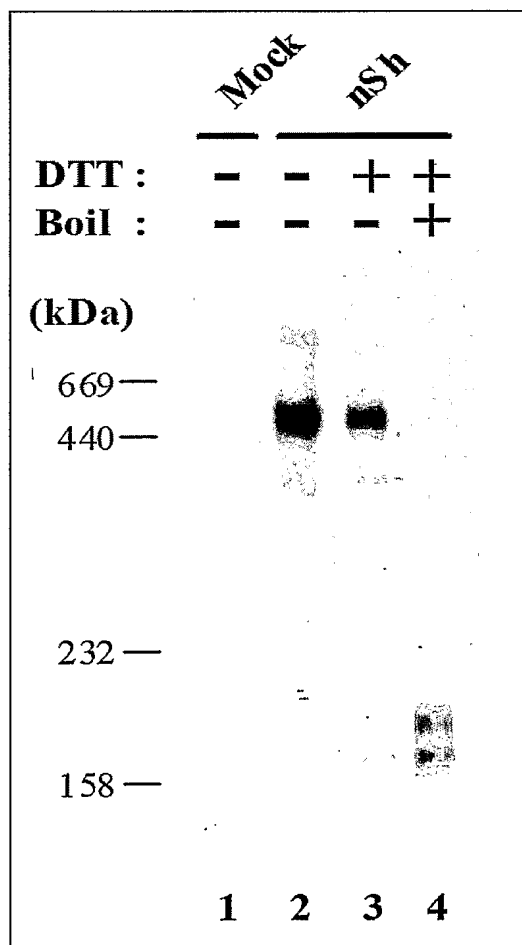
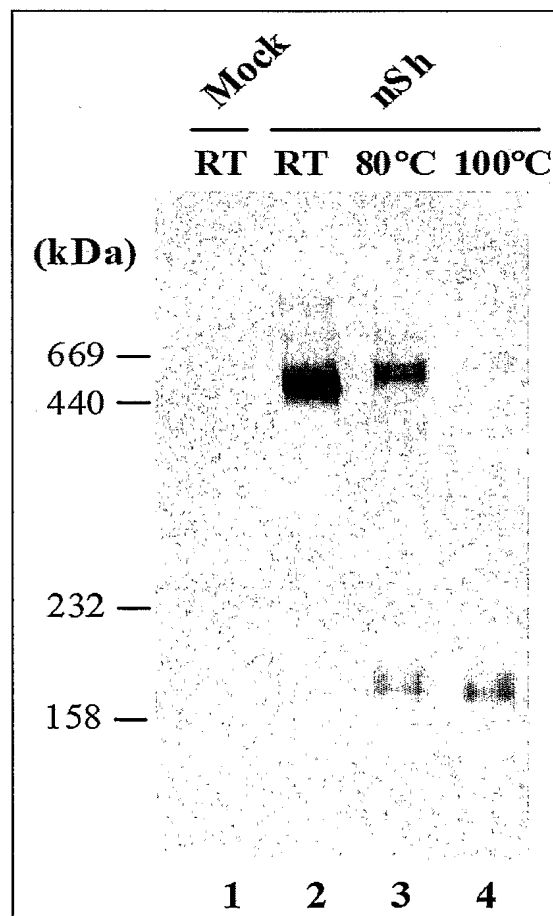


FIGURE 76**FIGURE 77****FIGURE 78**

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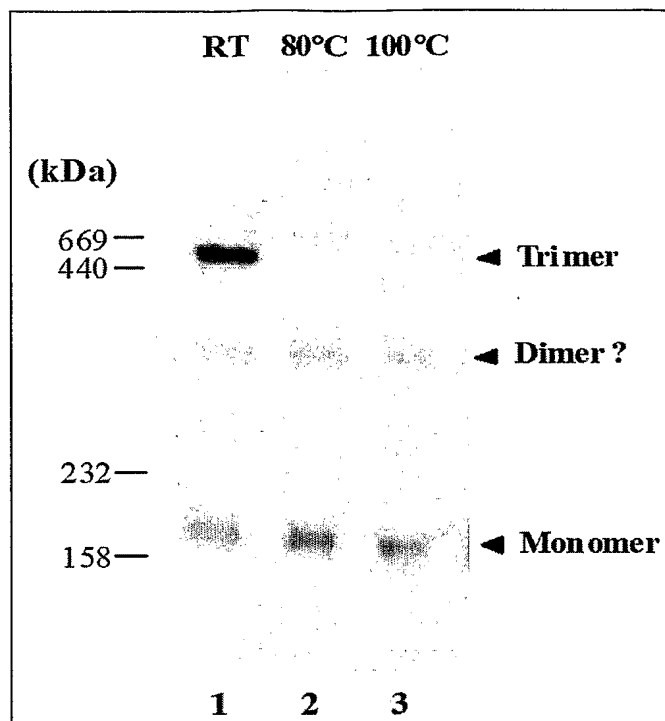
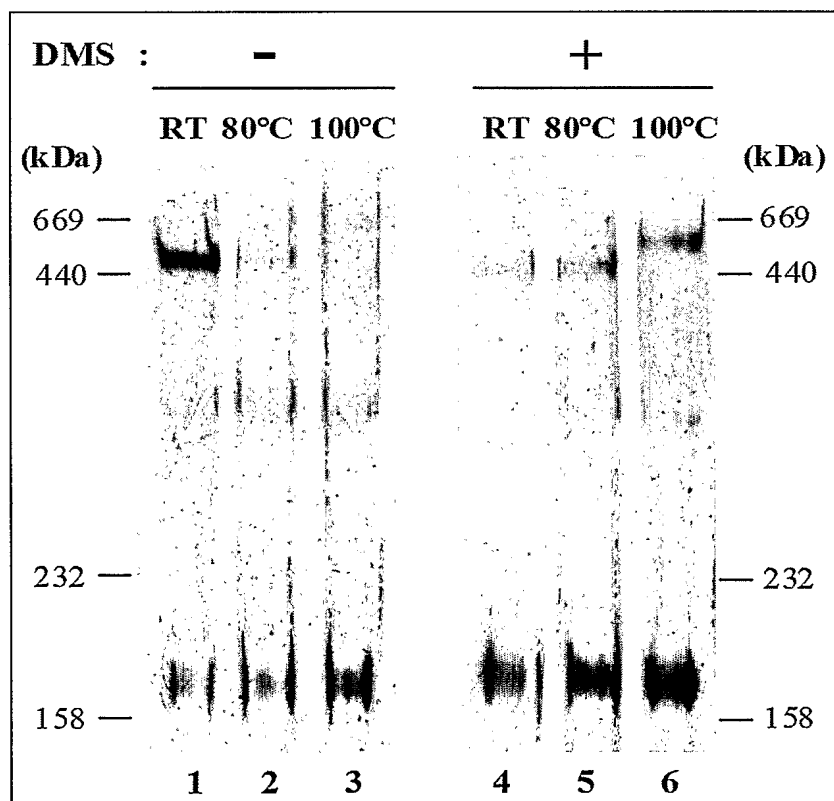
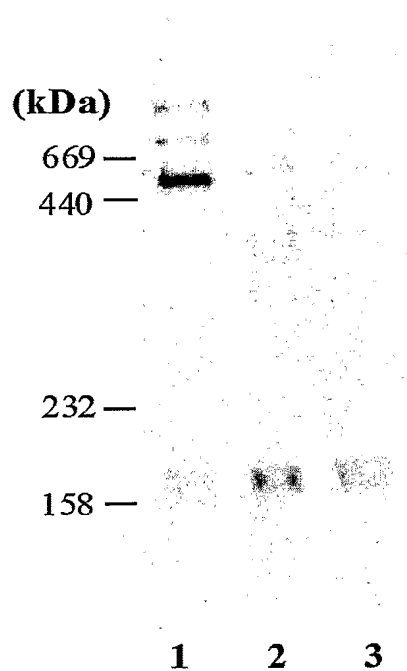
FIGURE 79**FIGURE 80**

FIGURE 81

RT 80°C 100°C

**FIGURE 82**

RT 80°C 100°C

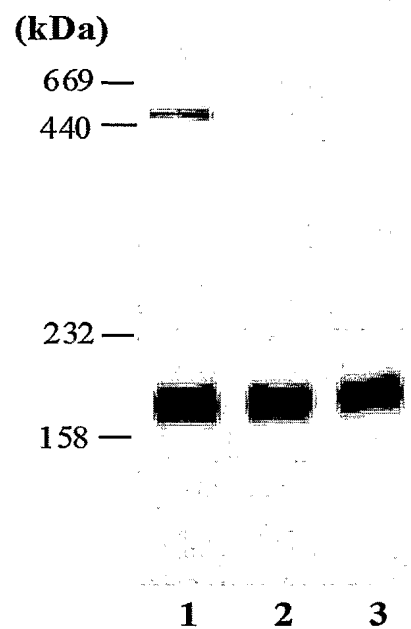
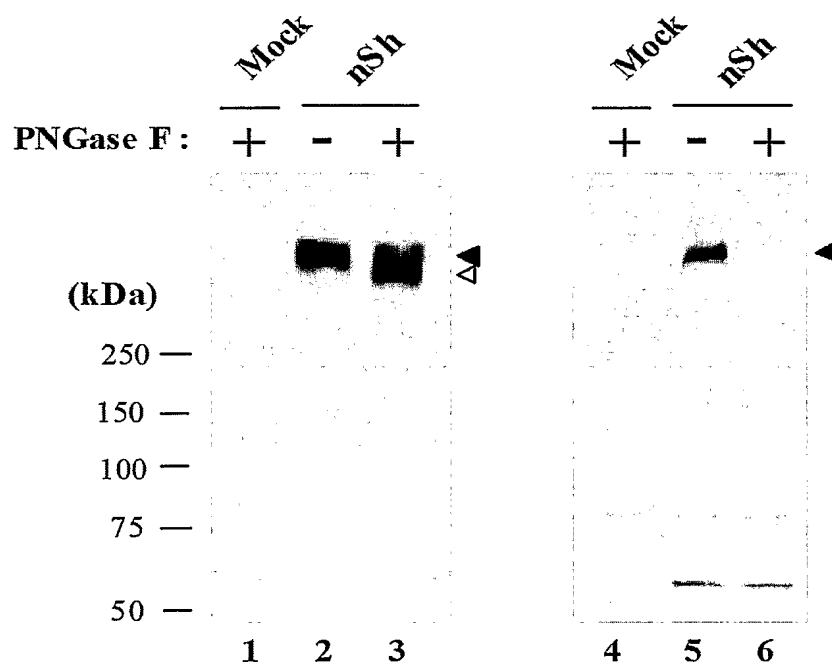
**FIGURE 83**

FIGURE 84

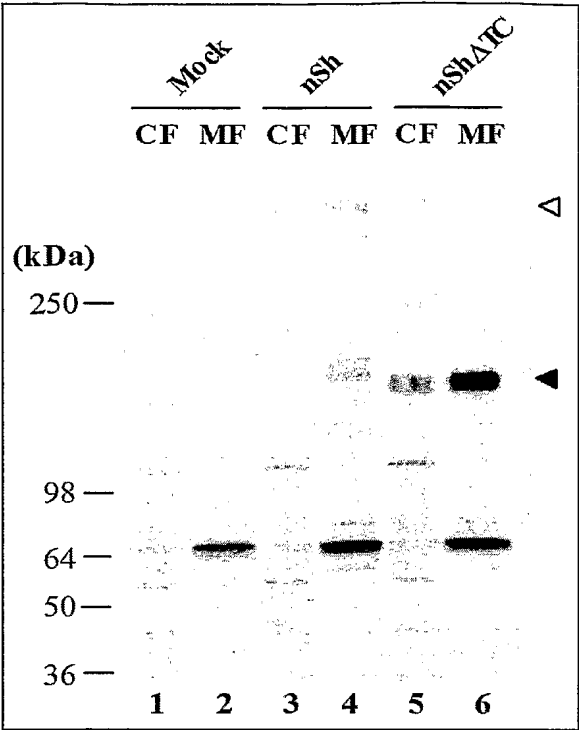


FIGURE 85

FIGURE 85A

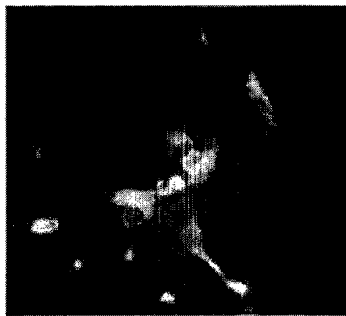


FIGURE 85B

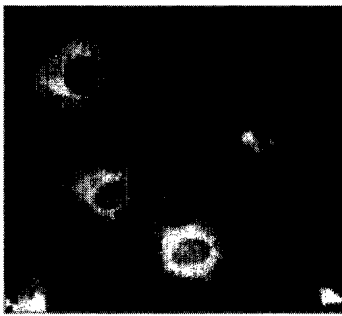


FIGURE 85C

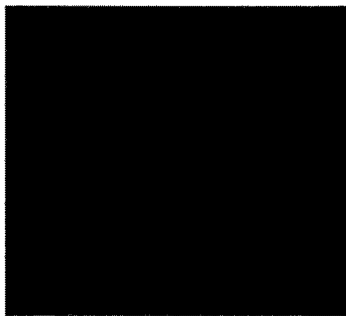


FIGURE 85E



FIGURE 85F



FIGURE 86

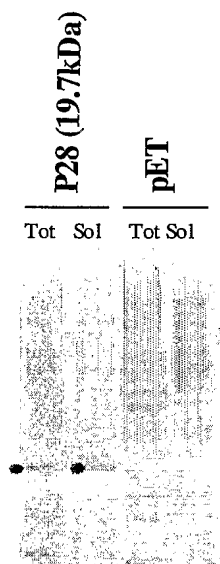


FIGURE 87

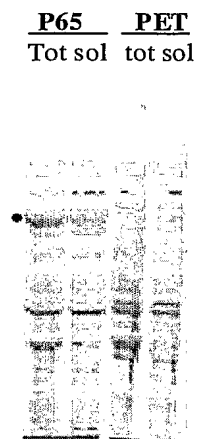


FIGURE 88

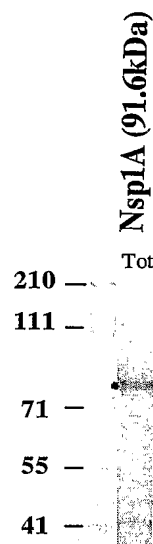


FIGURE 89

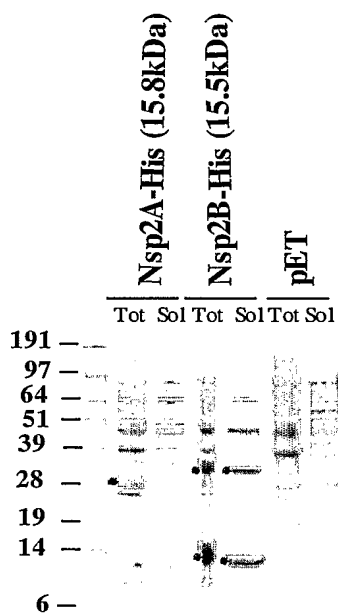


FIGURE 90

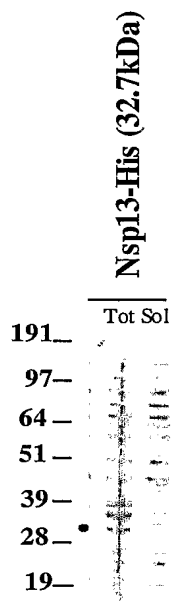


FIGURE 91

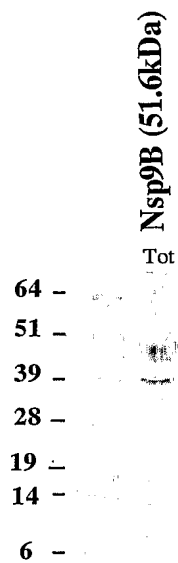


FIGURE 92

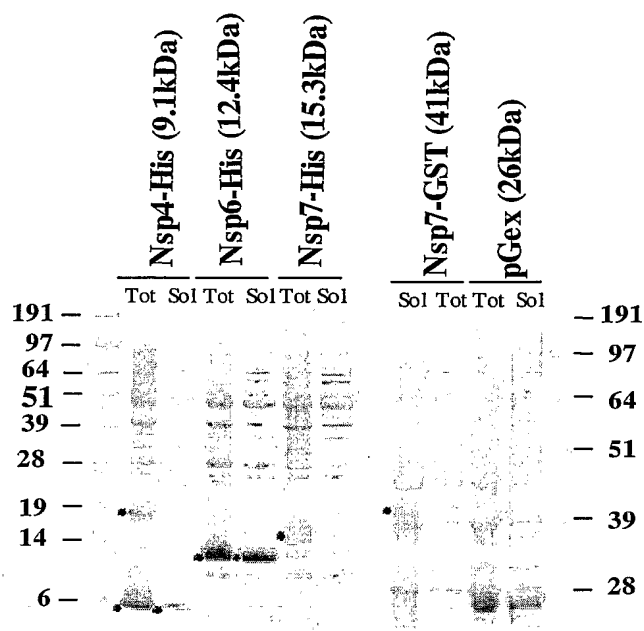


FIGURE 93

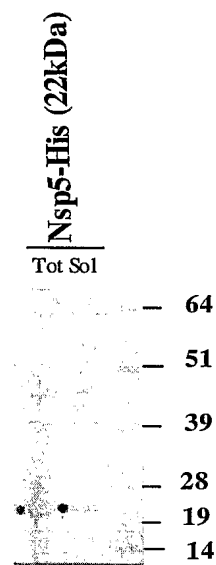


FIGURE 94

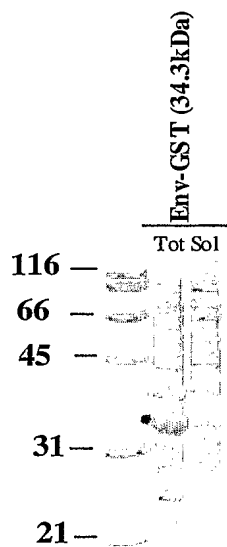


FIGURE 95

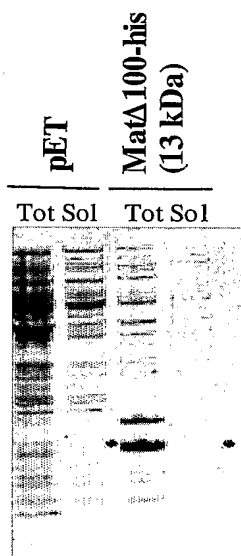


FIGURE 96

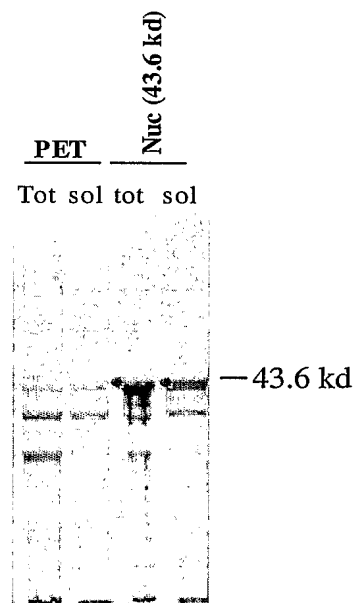


FIGURE 97

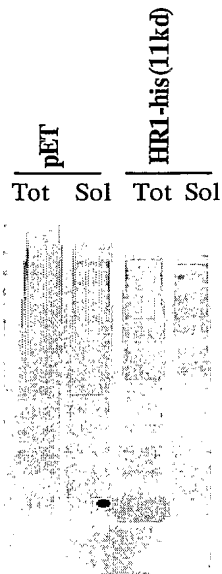


FIGURE 98

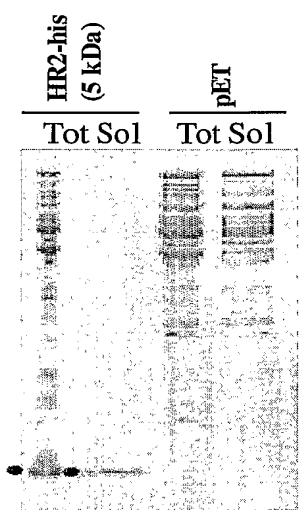


FIGURE 99

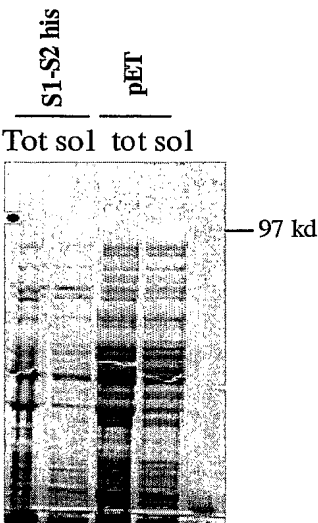


FIGURE 100

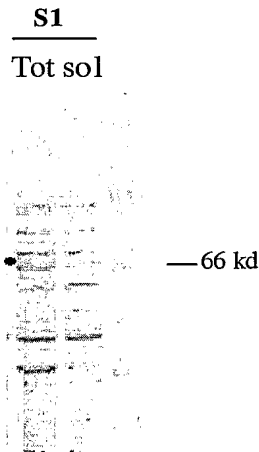


FIGURE 101

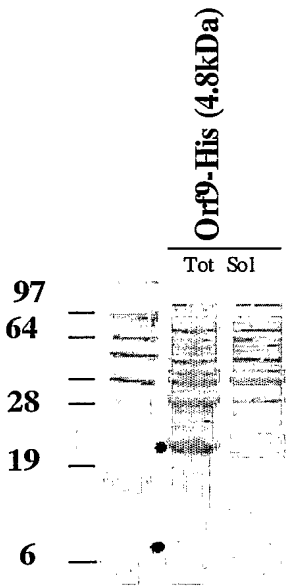


FIGURE 102

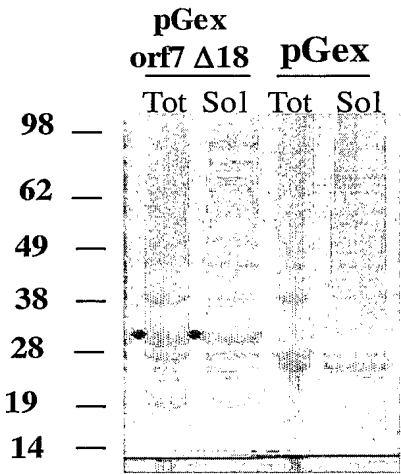


FIGURE 103

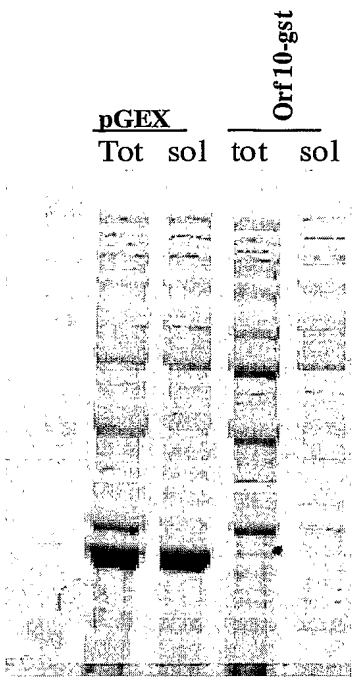


FIGURE 104



FIGURE 105

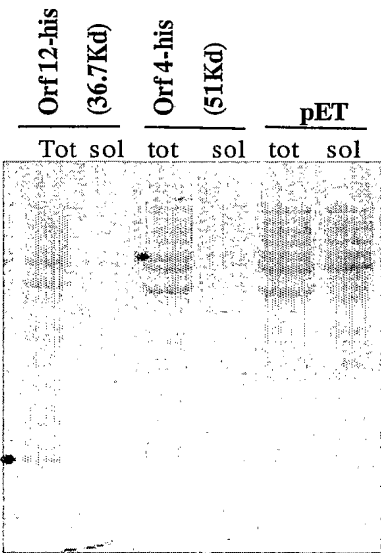


FIGURE 106

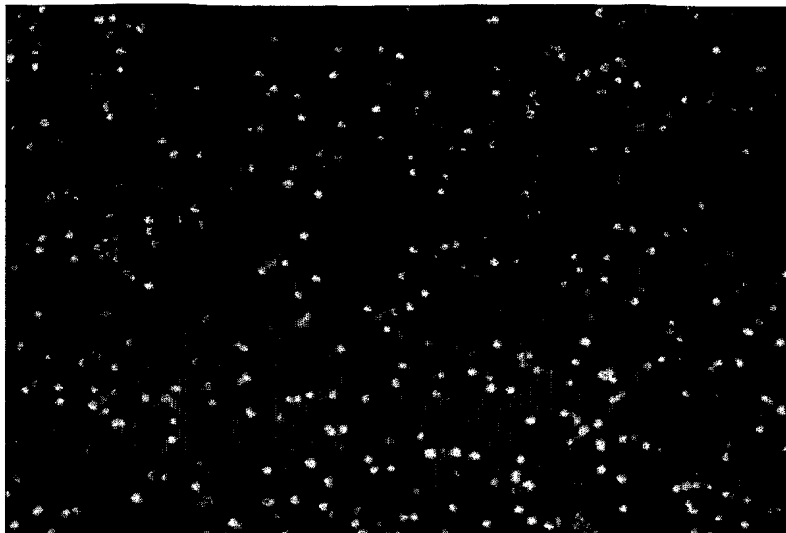


FIGURE 107

FIGURE 107A

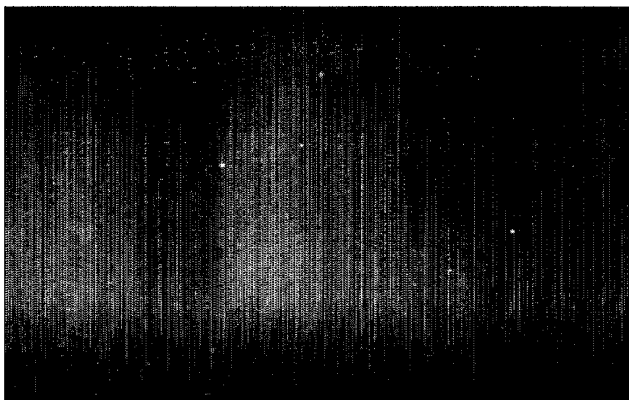


FIGURE 107B

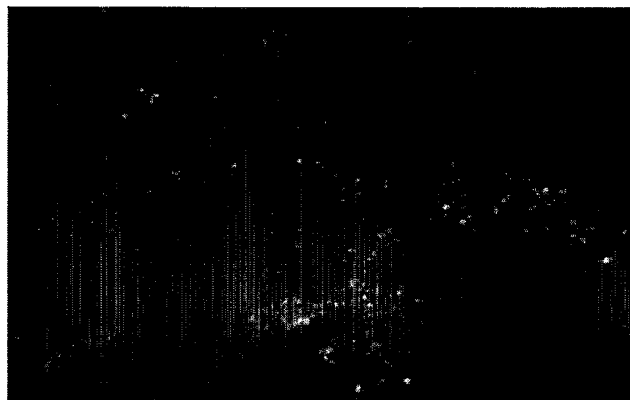


FIGURE 108

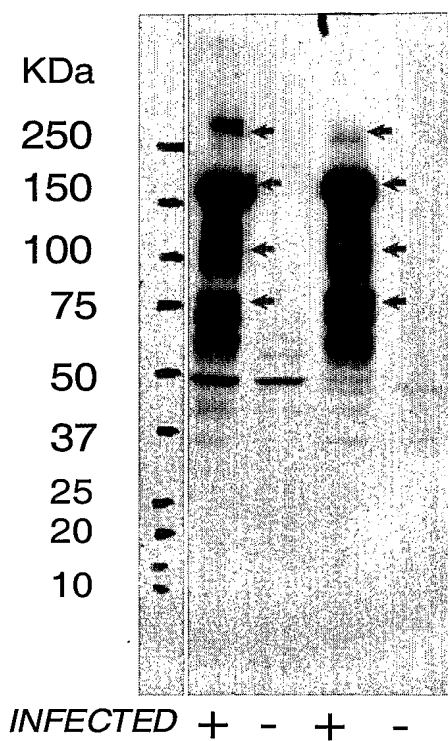
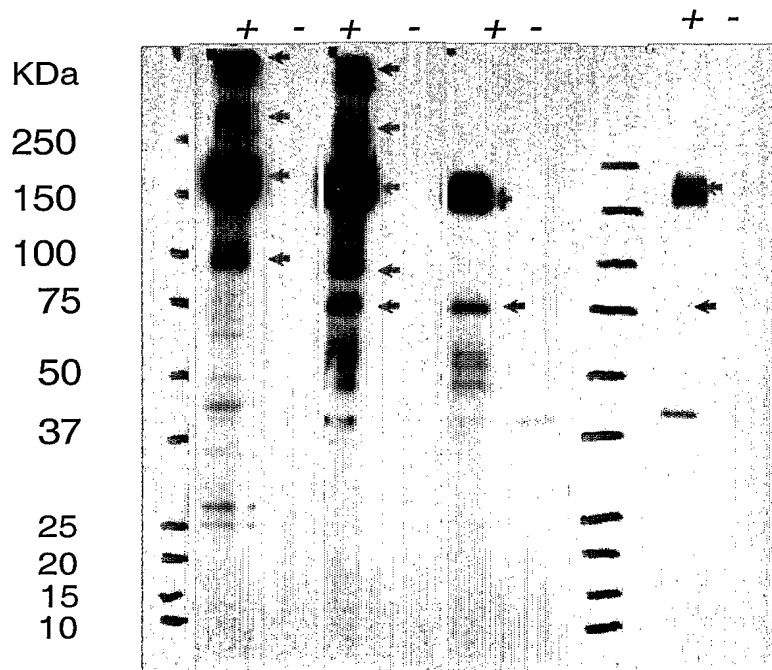
FIGURE 108A



FIGURE 108B



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FIGURE 109**S1 S1-S2****FIGURE 110****S1 S1-S2 HR2 HR1**

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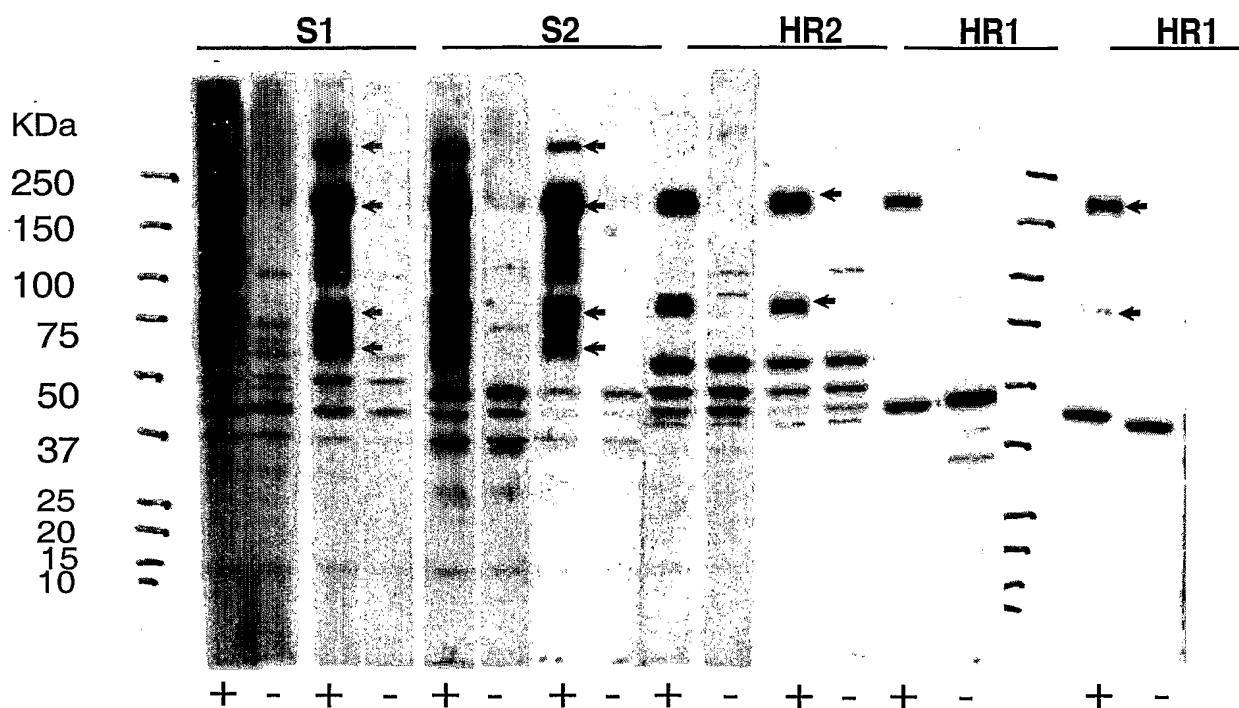
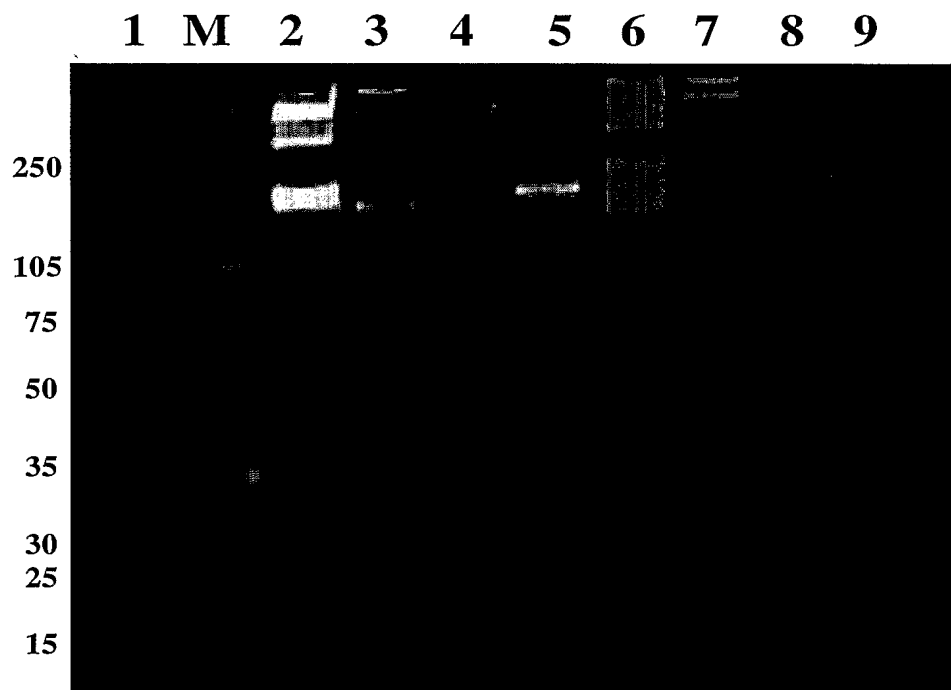
FIGURE 111**FIGURE 112**

FIGURE 113**5'3' Frame 1**

PKDMTYVDSSL-WVS-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYL
SS-DFLQVLT--LYRLVMLTLKITQNSPELMHKPPPVSLLNILYHSCIKACPGM-CVLR-
YKCSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKERVVCVTNVQLAFLHLHQILMPA
GIILWVLTMSITHL-LMFSSGGFTGNLSE-P-PTLPGTWKCTCGLVVML

5'3' Frame 2

QRT-PT-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PT
SPARIFYRC-LSSCTDWLC-H-K-HKIHQS-CTNLHQ-AV-TSYTTHV-RLALECSAY-D
STNAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNVLSV-QTCNLLFYFIRYLCL
LESFCGF-LCL-PIYD-CSAVGALRVTFQSNHDQHCQVHGNAHVG-L-C

5'3' Frame 3

KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP
LQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNVVRKI
VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYAC
WNHSGFDYVYNPFMIDVQQWGLYG-PFRVTMTNIARYMEMHMMWASCA

3'5' Frame 1

-HHN-PTCAFPTWQCWSWLL-KVTRKAPTAEHQS-MGYRHSQNPQNDSSRHKYLK-KS
KLHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTILSVYH-AFVLS-YALHSRAS
LYT-VV-DV-TAHWWRFVH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-L
HDSPLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYVGHVLW

3'5' Frame 2

SITTSPHVHFHVPGNVGHGYSERLPVKPPLLNINHKWVIDIVKTHRMIPAGISI--SRKA
SCTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QSFQCITEHLYYLNTHYIPGQA
FIHEWYKMFKLLTGGLCINSGEFCVIFSVNITSRYSY-VNTRKS-LER-VSTHSISSC
MTALYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHRDEST-VMSF

3'5' Frame 3

ASQLAHMCISMYLAMLMVTLKGYP-SPHC-TSIINGL-T-SKPTE-FQQA-VSDEVEKQ
VARLSHRQHVLSGPILTKYFIDVSSKPCAQRTNTTSLSDNPFVSVLSICTILIRTTFQGKP
LYMSGIRCLNCSLVEVCALTLVNFVLFVSVST-PVGTATKLTPVENPSWRGRLVPTASLVA
-QPSTSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLRRSCPL

FIGURE 114**5'3' Frame 1**

YRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLG
FSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLI

5'3' Frame 2

TVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-D
FLQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSLNILY

5'3' Frame 3

P-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PTSPARI
FYRC-LSSCTDWLC-H-K-HRIHQ5-CKTSTR-PV-TSYT

3'5' Frame 1

GIRCLNWSPGGGFALTLVNSVLF5VST-PVGTATKLTPVENPSWRGRLVPTASLVA-QPS
TSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLR

3'5' Frame 2

V-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-LHDSPL
HQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYG

3'5' Frame 3

YKMFKLVTWWRFCINSGEFCVIFSVNITSRY5Y-VNTCRKS-LER-VSTHSISSCMTALY
IKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDESTV

FIGURE 115**Section 151**

(5851) 5851 5860 5870 5889
 (5675) LTNYELSVINARIRAKHYVYIGDPAQLPAPRVLLSKGTL
 (5247) LTNYELSFINGKINYCYVVYVGDBAQLPAPRVLLING-SL
 (5762) LTNYELSVINSRYSARHYVYIGDPAQLPAPRVLLNEGTL
 (1) -----
 (5851) LTNYELSVINARI AKHYVYIGDPAQLPAPRVLLNKGTL

Section 152

(5890) 5890 5900 5910 5928
 (5714) EPKYENTVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV
 (5285) SPKDYNVVTNLMVCVKPDIFLAKCYRCPKEIVDTVSTLV
 (5801) EPRYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV
 (1) -----
 (5890) EPKYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV

Section 153

(5929) 5929 5940 5950 5967
 (5753) YDNKLKANNESSELCFKVYYKG ---VTTHESSESAVNMQQ
 (5324) YDGNFIANNPESRECFKVIIVNNGNSDVGHESGGSAYNTTQ
 (5840) YDNKLKARNDNSBMCFKVYYKG ---QTTHESSESAVNMQQ
 (1) -----
 (5929) YDNKLKAKND SSLCFKVYYKG TTHESSESAVNMQQ

Section 154

(5968) 5968 5980 5990 6006
 (5789) IYELINKELKANPLWHKAVETSPYNSQNF AAKRVLGLQTO
 (5363) LEFVKDEVCRNKQWREAFISPYNAMNQRAYRMLGLNVQ
 (5876) IHLISKELKANPSWSNAVFISPYNSQNYVAKRVLGLQTO
 (1) -----
 (5968) IHLI KFLKANP W AVFISPYNSQNF AKRVLGLQTO

Section 155

(6007) 6007 6020 6030 6045
 (5828) TVDSAQGSSEYDYVIYSQTAETAHSVNVNRFENVAITRAKK
 (5402) TVDSSQGSSEYDYVIFCVTADSQHAIINRENVALTRAKR
 (5915) TVDSAQGSSEYDEVYIYSQTAETAHSVNVNRFENVAITRAKK
 (1) -----
 (6007) TVDSAQGSSEYDYVIYSQTAETAHSVNVNRFENVAITRAKK

Section 156

(6046) 6046 6060 6070 6084
 (5867) GILCVMSNMQLFEALQFTTLTLDKVPQAVETRVQCSTNL
 (5441) GILVVMRQRDELYSALKFTELDQETS ----LQG ---TEL
 (5954) GILCVMSNMQLFESLNFTTLTLDKIN ---NPRLOCTTNL
 (1) -----
 (6046) GILCVMSNMQLFESLNFTTLTLDKI RLOQSTNL

START

FIGURE 115 (contd.)**Section 157**

(6085) 6085 6090 6100 6110 6123
 (5906) FKDCSKSYSGYHPAHAPSFLAVDDKYKATGDLAVELGIG
 (5473) EKICCKEFSGVHPAYAVTTKALAAATYKVNDELAPLVNVE
 (5990) EKDCSRSEYVGYPAHAPSFLAVDDKYKVGCDLAVCLNVA
 (1) -----
 (6085) FKDCSKSYSGYHPAHAPSFLAVDDKYKV GDLAVCLNVA

Section 158

(6124) 6124 6130 6140 6150 6162
 (5945) D-SAVTYSRLSEMGFILDVLDYCHL-LIKEH-VKR
 (5512) AGSEITTYRHL-LLIFMMSVIVE-CHNM-ITRDEAIR
 (6029) D-SAVTYSRLSEMGFILDVLDYCHL-ITRDEAIR
 (1) --KGHDLRPSEMGFIMSYQVNYENM-ITRDEAIR
 (6124) D SAVTYSRLISLMGFKLDVTLGDCNLFITRDEAIKRV

Section 159

(6163) 6163 6170 6180 6190 6201
 (5983) RA-VTFRDAGAH-TRDSITTHFSLQLPPTIDFVVEAT
 (5551) RG-V-EDVEATE-EGTNEHMLPPTV-ITDADEFVTR
 (6067) RA-VTFRDAGAH-TRDSITTHFSLQLPPTIDFVVEAT
 (38) TART-EDV-ET-TRDAVETTHFSLQLPPTVNL-VP
 (6163) RANVGEDVEGAHATRDSIGTNLPLQLGESTGIDFVVEPT

Section 160

(6202) 6202 6210 6220 6230 6240
 (6022) GLPADRDGYSEKKAVAKAPPGEQFKHLIPLMTRGQRTD
 (5590) GLVDTSIGNN-EPVNSKAPPGEQFKHLRVLEKSAFPWH
 (6106) LMFARDGYV-KKAAARAPPGEQFKHLPLMSRGQKWDV
 (77) LYVBTEHETKLRVNACTSTSEQFKHLIPLMYKGLPWH
 (6202) GLVDTRDGY FKKVNAKAPPGEQFKHLIPLMSRGQPWDV

Section 161

(6241) 6241 6250 6260 6279
 (6061) VRPRIVQMFADHLIDLSCVVL-TWAHFEITCLRYFVK
 (5629) LRPRIVQMLADNLCHVSDCFVFTWCHGLLTLRYFVK
 (6145) VRIRVQMLSLADLADLADL-TWAHFEITCLRYFVK
 (116) VRIRVQMLSLADLADLADL-TWAHFEITCLRYFVK
 (6241) VRPRIVQMLADHL DLSDCVVLVTWAHGFELTCLRYFVK

Section 162

(6280) 6280 6290 6300 6318
 (6100) VGRVISCNVCTKRAATAYNSRTGYGCVRHSTYTCYLVP
 (5668) IGRK-OVCS-IGGAAITENSHTQAAACVKKHCLGFLEVEN
 (6184) VGRVVDGVCTKRAATAYNSRTGYGCVRHSTYTCYLVP
 (155) IGRPERTEGLIDKFEITGFSTSSITVACNNHSTYTCYLVP
 (6280) IGRVISCNVCTKRAATAYNSRTGYGCVRHSTYTCYLVP

FIGURE 115 (contd.)**Section 163**

(6319)	6319	6330	6340	6357
(6139)	LIVDIQ	QNGYISLSSNHDLYCSVHKGAHVASSDAIMTR		
(5706)	LLVLI	QNGYISLSSNHDLYCSVHKGAHVASSDAIMTR		
(6223)	LIVDI	QNGYISLSSNHDLYCSVHKGAHVASSDAIMTR		
(194)	TMIDVQ	QNGYISLSSNHDLYCSVHKGAHVASSDAIMTR		
(6319)	LIVDIQ	QNGYISLSSNHDLYCSVHKGAHVASSDAIMTR		

Section 164

(6358)	6358	6370	6380	6396
(6178)	CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL			
(5745)	CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL			
(6262)	CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL			
(229)	-----			
(6358)	CLAVYDCFCNNINWNVEYPIISNELSINTSCRVLQRMVL			

Section 165

(6397)	6397	6410	6420	6435
(6217)	KAAMLCNRYTLCYDIGNPKAIACVKD--			
(5784)	NACVDALKVNVVYDIGNPKGIKCVRRGDVNEREYDKNPI			
(6301)	KAAMLCNRYTLCYDIGNPKAIACVKD--			
(229)	-----			
(6397)	KAAMLCNRYTLCYDIGNPKAIACVKD--			

Section 166

(6436)	6436	6450	6460	6474
(6254)	VKS VKTLLYSEEAHKDSEFKDGLCMFWNCNVDKYPNAV			
(5823)	VRNVKQFEYDYNQHKDKFADGLCMFWNCNVDKYPNAV			
(6338)	VKS VKTLLYSEEAHKDSEFKDGLCMFWNCNVDKYPNAV			
(229)	-----			
(6436)	VKS VKTLLYSEEAHKDSEFKDGLCMFWNCNVDKYPNAV			

Section 167

(6475)	6475	6480	6490	6500	6513
(6293)	CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE				
(5862)	CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE				
(6377)	CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE				
(229)	-----				
(6475)	CRFDTRVLN LNLP GCNGGSLYVNKHAFHTPKPFSRAAFE				

Section 168

(6514)	6514	6520	6530	6540	6552
(6332)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR				
(5901)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR				
(6416)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR				
(229)	-----				
(6514)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR				

FIGURE 115 (contd.)

Section 169

(6553)	6553	6560	6570	6580	6591
(6371)	CNIGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFD				
(5939)	CNIGGAVCKKHAQMYAEFVTSYNAAYTAGFTFWVTHLNM				
(6455)	CNIGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFD				
(229)	-----				
(6553)	CNIGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFD				

Section 170

(6592)	6592	6600	6610	6620	6630
(6410)	FYNLWNTFTKLOSLENNVYNLVKTGHYTGQAGEMPCAII				
(5978)	PYNLWKSFSALOSIDNIAYNMYKGCHYDAIAGEMPTVIT				
(6494)	FYNLWNTFTRLLOSLENNVYNLVNAGHFDGRAGELPCAVI				
(229)	-----				
(6592)	FYNLWNTFTKLOSLENNVYNLVKAGHYDG AGEMPCAII				

Section 171

(6631)	6631	6640	6650	6660	6669
(6449)	GDKVVAKIDKEDVVFINTTPTNVAVELFAKRSTRHH				
(6017)	GDKVVFVIDQGVKVFVNQTTLPSTVAFELYAKRNIRTL				
(6533)	GERVIAKIQNEDVVEKNNTTPTNVAVELFAKRSTRPH				
(229)	-----				
(6631)	GDKVIAKIQ EDVVVFINTTPTPTNVAVELFAKRSIR H				

Section 172

(6670)	6670	6680	6690	6700	6708
(6488)	PELKLFRNLNIDVCWKHVIWDYARESTFCSNTYGVCMYT				
(6056)	PNNRLKRLCVDVTNGFVIWDYALCTPIYRNTVKVCAYT				
(6572)	PELKLFRNLNIDVCWSHVLWDYAKDSVECSSTYKVCXYT				
(229)	-----				
(6670)	PELKLFRNLNIDVCW HVIWDYAKDSIFCSNTYKVC YT				

Section 173

(6709)	6709	6720	6730	6740	6747
(6527)	DLKFEDKLNVLFDGRDNGALEAFKRSNNGVYISTTKVKS				
(6095)	DIEFNG--LWVLYDDRYGDYCSFLAADNAVLMSTQCCKR				
(6611)	DLQCFESLNVLFDRDNGALEAFKRSNNGVYINTTKIKS				
(229)	-----				
(6709)	DL ID LNVLFDRDNGALEAFKKA NGVYISTTKIKS				

Section 174

(6748)	6748	6760	6770	6780	6786
(6566)	LSMIKGPRAELNGVVVDKVGSDTDCVFFAVRKEGQDVI				
(6132)	YSYVEIPSNNLLVQNGMPLKDG-----ANLYV				
(6650)	LSMIKGPORADLNGVVVEKVGSDSDFWFVAVRKEGQDVI				
(229)	-----				
(6748)	LSMIKGP RADLNGVVVDKVGSD FWFVAVRKDGNDVI				

SEQ ID NO: 10068

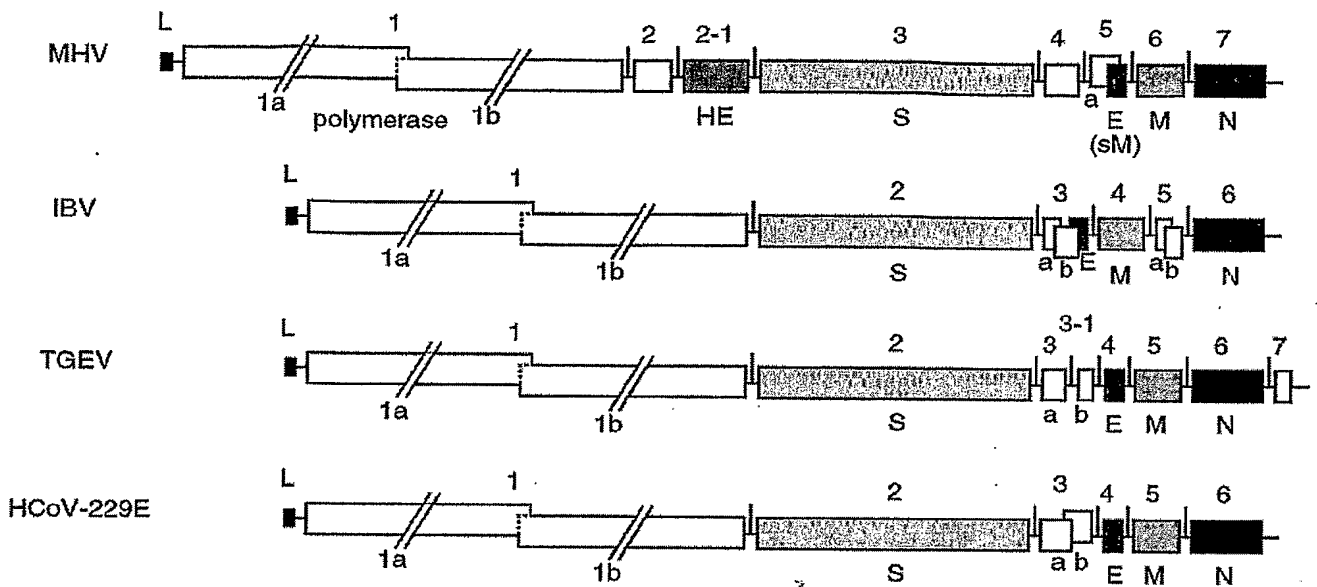
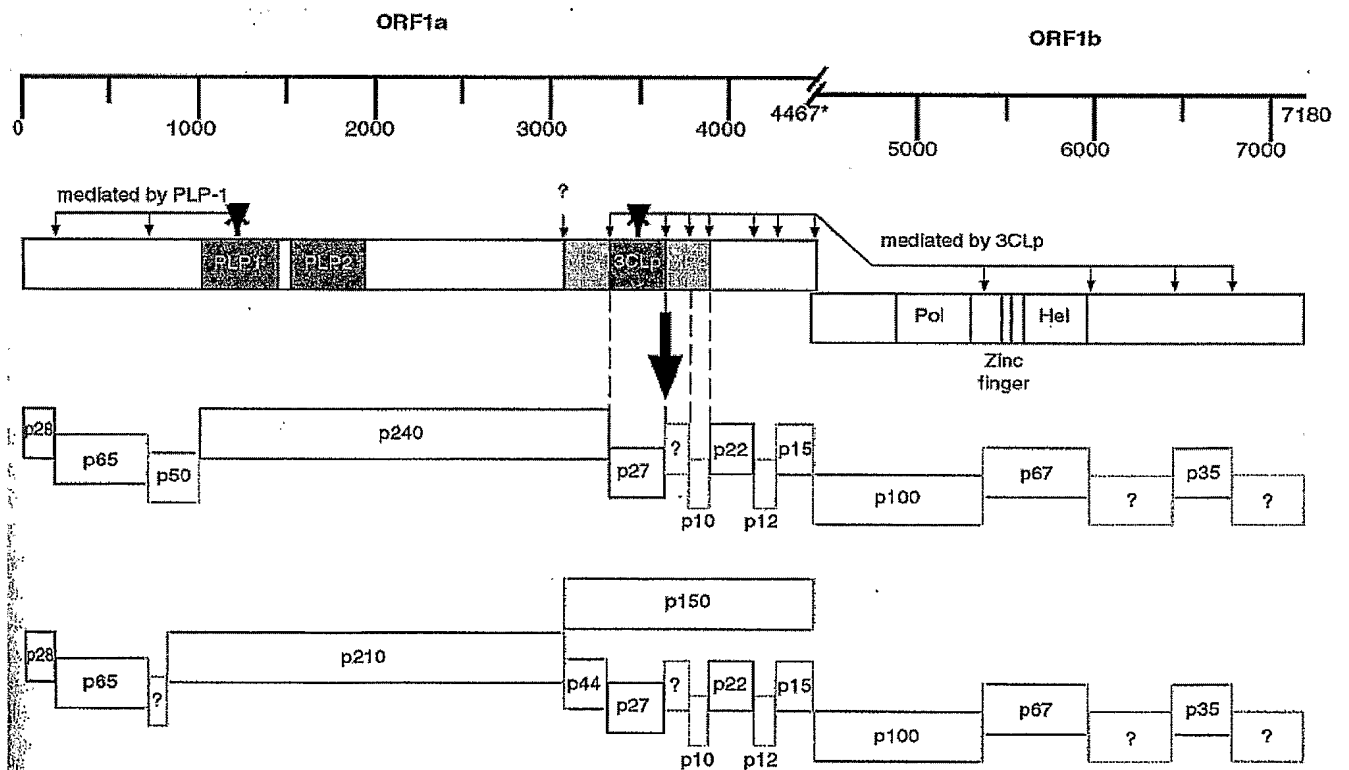
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SEQ ID NO: 10070

SEQ ID NO: 9997/98

SEQ ID NO: 10071

141/193

FIGURE 116**FIGURE 117**

“*”

FIGURE 118

Section 1					
(1)	1	10	20	30	40
(1)	-GAGGIFKIQNKEEESGVHPYVETKRLAATLVNDELALVNVEAGM				
(1)	CSTNLFEDSKSYSYPAHPSFLVDDKLRATGDLVCLCIGD-KHFDL				
(1)	CTTNLFEDSRSYVLYHPAHPSFLVDDKLVGGDLVCLNVAD-KGHDL				
(1)	CSTNLFEDSKSYSYPAHPSFLVDDKLVGGDLVCLNVAD-KHFDL				
(1)	CSTNLFKDCSKSYSGYHPAHAPSFLAVDDKYKVGGDLAVCLNVAD KGHDL				
Section 2					
(52)	52	60	70	80	90
(51)	RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG				
(51)	RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG				
(51)	RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG				
(51)	RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG				
(52)	RRLISMGMGEKMN YQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG				
Section 3					
(103)	103	110	120	130	140
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM				
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM				
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM				
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM				
(103)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM				
Section 4					
(154)	154	160	170	180	190
(153)	YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE				
(153)	YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE				
(153)	YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE				
(153)	YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE				
(154)	YKGLPWNVVRRIKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE				
Section 5					
(205)	205	210	220	230	240
(204)	RTCCLCDKCRATCFSTSSDTYACWNHSGFDYVYNPFMIDVQQWGLYGSLS				
(204)	RTCCLCDKCRATCFSTSSDTYACWNHSGFDYVYNPFMIDVQQWGLYGSLS				
(204)	RTCCLCDKCRATCFSTSSDTYACWNHSGFDYVYNPFMIDVQQWGLYGSLS				
(204)	RTCCLCDKCRATCFSTSSDTYACWNHSGFDYVYNPFMIDVQQWGLYGSLS				
(205)	RTCCLCDKCRATCFSTSSDTYACWNHSGFDYVYNPFMIDVQQWGLYGSLS				
Section 6					
(256)	256	270	280	290	306
(255)	NHDHLHCSVHKGAVHASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN				
(255)	NHDLYCSVHKGAVHASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN				
(255)	NHDPICSVHKGAVHASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN				
(255)	NHDHLHCSVHKGAVHASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN				
(256)	NHDHLHCSVHKGAVHASSDAIMTRCLAVHDCFCNSVWNWNLBYPIISNELSVN				

FIGURE 118 (contd.)**Section 7**

(307) 307	320	330	340	357
(306) SPFTYLDEMYLNALMDALKVNVVLEDEPAGLKVRRGQVNTERTTEKNEIM				
(306) TSCQVLDQVMLKAAMLCNRYTLCYDIGNPKGIACVK--DFDEKFIYDAQELIV				
(306) TSCQLLDQVMERAAMLCNRYDVCCYDIGNPKGIACVK--GYDEKFIYDAQELIV				
(306) TSCQLLDQVMLKAAMLCNRYTVCCYDIGNPKGIACVK--DFDEKFIYDAQELIV				
(307) TSCRLLRVMLKAAMLCNRYTVCCYDIGNPKGIACVK				DFDEKFIYDANPIV

Section 8

(358) 358	370	380	390	408
(357) RNVKQFELYDYNQHKDKFADGLCMFWNCNVDCYFDNSLVCRDYDTPNLSVFNL				
(355) KSVKTLLEYSEEAHKDSFKDGLCMFWNCNVDKYFPNAVVCREDTRVLNNLNL				
(355) KSVKQFVYKYEAHKDQFLDGLCMFWNCNVDKYFPNAVVCREDTRVLNKLNL				
(355) KSVKQELYSYEAHKDSFKDGLCMFWNCNVDKYFPNAVVCREDTRVLN-LNL				
(358) KSVKQFLYSYEAHKDSFKDGLCMFWNCNVDKYFPNAVVCREDTRVLN				LNL

Section 9

(409) 409	420	430	440	459
(408) PCGNGGSLYVNHAFHTKPFSSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ				
(406) PCGNGGSLYVNHAFHTKPFSSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ				
(406) PCGNGGSLYVNHAFHTKPFSSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ				
(405) PCGNGGSLYVNHAFHTKPFSSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ				
(409) PGCNGGSLYVNHAFHTKPFSSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ				

Section 10

(460) 460	470	480	490	500	510
(458) QLYSLATKDEITKQNTGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT					
(457) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT					
(457) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT					
(456) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT					
(460) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT					

Section 11

(511) 511	524	
(509) LDFYNLWNTFTKLQ	SEQ ID NO: 10073	
(508) FDFYNLWNTFTKLQ	SEQ ID NO: 10074	
(508) FDFYNLWNTFTKLQ	SEQ ID NO: 10075	
(507) FDFYNLWNTFTKLQ	SEQ ID NO: 10076	
(511) FDFYNLWNTFTKLQ	SEQ ID NO: 10077	

FIGURE 119

tagtcaaaacccacagaatgattccagcaggcataagtatctgatgaagtagaaaagcaa
 - - - V S D E V E K Q
 gttgcacgt**TTG**tcacacagacaacacggttctttcaggtccaatc**TTG**acaaagtacttc
 V A R L S H R Q H V L S G P I L T K Y F
 attgatgtaagctcaaagccatgcgcccaaaggacgaacacgactctgtctgacaatcct
 I D V S S K P C A Q R T N T T L S D N P
 ttcagtgtatcactgagcatttgtactatcttaatacgcactacattccagggcaagcct
 F S V S L S I C T I L I R T T F Q G K P
 ttatac**ATG**agtgggtataagatgtttaactgctcactgggtggaggtttgtgcattaact
 L Y M S G I R C L N C S L V E V C A L T
 Ctggtgaattttgtgttattttcagtgtcaacataa **SEQ ID NO: 10080**
 L V N F V L F S V S T - **SEQ ID NO: 10027**

FIGURE 120**FIGURE 120A**

PRHTQRT-PTVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQ
 LEMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSNLILYH
 SCIKACPGM-CVLR-YKCSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKER
 VVCVTNVQLAFLHQLMPAGIILWVLTMSITHL-LMFSSGALRVTFRVMTNIA
 RYMEMHMLVVMLS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLAKEYNTWL
 -SLHCLLISFQFFMT-EIQRLSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILML
 YITINSLMVFCFIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVCM-ISMHS
 TLQLSIKVHLLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VV
 LFADTMQMSTDSTWMHII--FLLDLAYGFTNNLILITCGIHLPGYRV

FIGURE 120B

LGIPKGHDLP-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN
 -RCCGY-PTSPARIFYRC-LSSCTDWLC-H-K-HRIHQ-SCKTSTR-PV-TSYTT
 HV-RLALECSAY-DSTNAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNV
 LSV-QTCNLLFYFIRYLCLLESFCGF-LCL-PIYD-CSAVGLYG-PSE-P-PTLP
 GTWKCTCG-L-CYHD-MFSSP-VLC-AR-LVC-IPYYRR-TEG-FCLQKSTTHGC
 EVCIA--VSSSS-HRKSKEYQVCASG-SRMEVLRC SAM--QSLQNRGTLLFLCY
 TSR-IH-WCLFVLEL-R-SLPSQCNCV-V-HKSLVKLELTRL-WW-FVCE-ACIP
 HSSFR-KCIY-FKAIAFLLLF--SL-VSWQTSSVGY-LCSTQICYVYYTMQFRWC
 CLQTPCK-VPTVLGCI-YDDFCWI-PMDLQTI-YL-PVEYIYQVTEF

FIGURE 120C

-AYPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG
 TNLPLQLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVV
 RIKIVQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD
 TYACWNHSGVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAV
 HECFVKRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVF
 QAEVEWKFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVD RYPANAIVCRFD
 TRVLSNLSNLP GCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSD
 IDYVPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNT
 FTRLQSL

FIGURE 120D

-TL-PGKCIPQVISIKLFVNP-AKSSRNHHIICIQVLSVLICMV SANSTT-IASCNTRSR
 FEWNIINIRHYLFAMRLTRTIRIVKERQLL-ISKCTFIESWSVECM LIHIQT TTITAW-V
 QV-QDSCVKPTHNCIGWVTINVTIPKQNTISEFIVMYSIRIEEFLYFVSFVTTWLSIVE
 LPFYFSLRHTLDSLWISYVMKNWKLI SKQCRLHNHVLYFSASRINPQFISYNRVFNRPIN
 ALNKALMDC-TSSHDSITTSHMCISMYLAMLVMVTLKVTRKAPLLNINHKKWVIDIVKTHR
 MIPAGISI--SRKASCTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QSFQCITE
 HLYYLNTHYIPGQAFIHEWYKMFKLVTWWRFCINSGEFCVIFSVNITSRYSY-VNTCRKS
 -LER-VSTHSISSCMTALYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDESTVG
 HVLWVCL

FIGURE 120E

KLCNLVN VFHRL-VSNCL-IHRLNPAEIIILYASKYCRY SFAWCLQTAPPKLHRVIVHAD
 LSGT-SISDTTCLP-DSQGLSE--KKGNCFKLVNALLSKAGVWNACLF TYKLPPSQPGKF
 KFDKTLVSNLHTIALAG-RSTLQFQNKQTPSVNLS-CIA-E-KSSSIL-ALSLHG-AS-N
 FHSTSA-GTHLIAFGFPMS-RTGNLSASNADFTTMCCTFLQAE LTLSSSPIIGYSTDQST
 RLTKHSWTAKHLVMIASQLATCAFPCTWQCWSWLL-RLPVKPHC-TSIINGL-T-SKPTE
 -FQQA-VSDEVEKQVARLSHRQHVLSGPILTKYFIDVSSKPCAQRTNTT LSDNPF SVLS
 ICTILIRTTFQ GKPLYMSGIRCLNWSPGGGFALT LVNSVLFSVST-PVGTATKLTPVENP
 SWRGRLVPTASLVA-QPSTSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLR-V
 MSFGYA-

FIGURE 120F

NSVTW-MYSTGYKYQIVCKSIG-IQKSSYYMHPSTVGTHLHGVC KQHHLNCIV-YT-QI
 -VEHNQYPTLLVCHETHKDYQNSKRKAIALN--MHFYRKLECGMHAYSHTNYHHHSLVSS
 SLTRL LCQTYTQLHWLGNDQRYNSKTNKHHQ-IYRDV-HKNRRVPLFCKLCHYMAEHRRT
 SILLQPEAHT--PLDFLCHEELETYQQAMQTSQPCVVLFCCKQN-PSVHLL--GIQQTNQR
 A-QSTHGLLNI-S--HHN-PHVHFHVPGNVGHGYSEGYP-SPTAEHQ S-MGYRHSQNPQN
 DSSRHKYLK-KSKLHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTILSVYH-A
 FVLS-YALHSRASLYT-VV-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS-HL-KIL
 AGEVG-YPQHL-LHDSPLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYGRS
 CPLGMPR

FIGURE 121

	10	20	30	40	50	60
SEQ ID NO:10033	-----TACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
SEQ ID NO:10084	CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
Consensus	TACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
Prim. cons.	CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
	70	80	90	100	110	120
SEQ ID NO:10033	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC					
SEQ ID NO:10084	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC					
Consensus	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC					
Prim. cons.	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTC					
	130	140	150	160	170	180
SEQ ID NO:10033	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
SEQ ID NO:10084	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
Consensus	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
Prim. cons.	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
	190	200	210	220	230	240
SEQ ID NO:10033	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
SEQ ID NO:10084	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
Consensus	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
Prim. cons.	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
	250	260	270	280	290	300
SEQ ID NO:10033	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
SEQ ID NO:10084	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
Consensus	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
Prim. cons.	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
	310	320	330	340	350	360
SEQ ID NO:10033	CAGGTGACCAGTTTAAACATCTTATACC-----					
SEQ ID NO:10084	CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG					
Consensus	CAGGTGACCAGTTTAAACATCTTATACC					
Prim. cons.	CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG					

etc.

FIGURE 122**5'3' Frame 1**

cctaggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaa
P R H T Q R T - P T V D S S L - W V S K
tgaattaccaagtcaatgggttaccctaatatgtttatcacccgcgaagaagctattcgtc
- I T K S M V T L I C L S P A K K L F V
acgttcgtgctggattggcctttgatgtagagggctgtcatgcaactagagatgctgtgg
T F V R G L A L M - R A V M Q L E M L W
gtactaacctacctctccagctaggattttctacaggtgttaacttagtagctgtaccga
V L T Y L S S - D F L Q V L T - - L Y R
ctggttatgttgacactgaaaataaacacagaattcaccagaggttaatgcaaacctccac
L V M L T L K I T Q N S P E L M Q N L H
caggtgaccagtttaaacatcttataccactcatgtataaaggccttgccctggaatgtag
Q V T S L N I L Y H S C I K A C P G M -
tgcgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcg
C V L R - Y K C S V I H - K D C Q T E S
tgttcgtcctttgggcgcgatggcctttgagcttacatcaatgaagtactttgtcaagattg
C S S F G R M A L S L H Q - S T L S R L
gacctgaaagaacgtgtttgtctgtgtgacaaacgtgcaacttgcttttctacttcatcag
D L K E R V V C V T N V Q L A F L L H Q
atacttatgcctgctggaatcattctgtgggttttgactatgtctataaccatttatga
I L M P A G I I L W V L T M S I T H L -
ttgatgttcagcagtggggctttacgggtaaccttcagagtaaccatgaccaacattgcc
L M F S S G A L R V T F R V T M T N I A
aggtacatggaaatgcacatgtggctagttgtgatgctatcatgactagatgttttagcag
R Y M E M H M W L V V M L S - L D V - Q
tccatgagtgcctttgttaagcgcgttgattgggtctgttgaataccctattataggagatg
S M S A L L S A L I G L L N T L L - E M
aactgaggggttaattctgcttgcaaaaagtacaacacatggttgtgaagtctgcattgc
N - G L I L L A E K Y N T W L - S L H C
ttgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgc
L L I S F Q F F M T - E I Q R L S S V C
ctcaggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttaca
L R L K - N G S S T M L S H V V T K L T
aaatagaggaactcttctatttcttatgctatacatcacgataaattcactgatgggtgttt
K - R N S S I L M L Y I T I N S L M V F
gtttgttttgggaattgtaacggttgatcggttaccagccaatgcaattgtgtgtaggtttg
V C F G I V T L I V T Q P M Q L C V G L
acacaagagtcttgtcaaaacttgaacttaccaggctgtgatgggtgtagtttgtatgtga
T Q E S C Q T - T Y Q A V M V V V C M -
ataagcatgcattccacactccagcttttcgataaaaagtgcatttactaatttaaagcaat
I S M H S T L Q L S I K V H L L I - S N
tgccttttcttttactatttctgatagtccttgtgagtcctcatggcaaacaagtagtgctcg
C L S F T I L I V L V S L M A N K - C R
atattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtg
I L I M F H S N L L R V L H D A I - V V
ctgtttgcagacaccatgcaaatgagtaccgacagtacttggatgcatataatatgatga
L F A D T M Q M S T D S T W M H I I - -
tttctgctggatttagcctatggatttacaacaatttgatacttataacctgtggaata
F L L D L A Y G F T N N L I L I T C G I

catttaccaggttacagagttta
H L P G Y R V

5'3' Frame 2

cctagggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaat
L G I P K G H D L P - T H L Y D G F Q N
gaattaccaagtcaatgggttaccctaatatgtttatcacccgcgaagaagctattcgtca
E L P S Q W L P - Y V Y H P R R S Y S S
cgttcgtgcggtgattggccttgatgtagagggctgtcatgcaactagagatgctgtggg
R S C V D W L - C R G L S C N - R C C G
tactaacctacctctccagctaggatcttctacaggtgttaacttagtagctgtaccgac
Y - P T S P A R I F Y R C - L S S C T D
tggttatgttgacactgaaaataacacagaattcaccagagttaatgcaaaacctccacc
W L C - H - K - H R I H Q S - C K T S T
aggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccctggaatgtagt
R - P V - T S Y T T H V - R L A L E C S
gcgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgt
A Y - D S T N A Q - Y T E R I V R Q S R
gttcgtcctttgggcgcgtggttggagcttacatcaatgaagtactttgtcaagattgg
V R P L G A W L - A Y I N E V L C Q D W
acctgaaagaacgtgttgctgtgtgacaaacgtgcaacttgcttttctacttcatcaga
T - K N V L S V - Q T C N L L F Y F I R
tacttatgcctgctggaatcattctgtgggttttgactatgtctataacccatttatgat
Y L C L L E S F C G F - L C L - P I Y D
tgatgttcagcagtggggctttacgggtaaccttcagagtaacctatgaccaacattgcca
- C S A V G L Y G - P S E - P - P T L P
ggtacatggaaatgcacatgtggctagttgtgatgctatcatgactagatgttttagcagt
G T W K C T C G - L - C Y H D - M F S S
ccatgagtgctttgttaagcgcgttgattgggtctgttggaataccctattataggagatga
P - V L C - A R - L V C - I P Y Y R R -
actgagggttaattctgcttgcagaaaagtacaacacatgggtgtgaagctctgcattgct
T E G - F C L Q K S T T H G C E V C I A
tgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgcc
C - - V S S S S - H R K S K G Y Q V C A
tcaggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttaciaa
S G - S R M E V L R C S A M - - Q S L Q
aatagaggaactcttctattcttatgctatacatcacgataaattcactgatgggtgttg
N R G T L L F L C Y T S R - I H - W C L
tttgttttgggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttga
F V L E L - R - S L P S Q C N C V - V -
cacaagagtcttgtcaaacttgaacttaccaggctgtgatgggtgtagtttgtatgtgaa
H K S L V K L E L T R L - W W - F V C E
taagcatgcattccacactccagcttttcgataaaagtgcatttactaatttaaagcaatt
- A C I P H S S F R - K C I Y - F K A I
gcctttcttttactattctgatagtccttgtgagtctcatggcaaacaagtagtgctcgga
A F L L L F - - S L - V S W Q T S S V G
tattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtgc
Y - L C S T Q I C Y V Y Y T M Q F R W C
tgtttgcagacaccatgcaaatgagtaccgacagtagtcttggtatgcatataatatgatgat

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C L Q T P C K - V P T V L G C I - Y D D
 ttctgctggatttagcctatggattttacaaacaatttgatacttataacctgtggaatac
 F C W I - P M D L Q T I - Y L - P V E Y
 atttaccagggttacagagtta
 I Y Q V T E F

5'3' Frame 3

cctaggcataccacaaaggacATGacctaccgtagactcatctctatgatggggtttcaaaatg
 - A Y P K D M T Y R R L I S M M G F K M
 aattaccaagtcaatgggttacctaataatgtttatcacccgcgaagaagctattcgtcac
 N Y Q V N G Y P N M F I T R E E A I R H
 gttcgtgctggattgggtttgatgtagagggctgtcatgcaactagagatgctgtgggt
 V R A W I G F D V E G C H A T R D A V G
 actaacctacctctccagctaggattttctacagggtgttaacttagtagctgtaccgact
 T N L P L Q L G F S T G V N L V A V P T
 gggtatgttgacactgaaaataacacagaattcaccagagttaatgcaaaacctccacca
 G Y V D T E N N T E F T R V N A K P P P
 ggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccttggaatgtagtg
 G D Q F K H L I P L M Y K G L P W N V V
 cgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgtg
 R I K I V Q M L S D T L K G L S D R V V
 ttcgtcctttgggcgcagtggtttgagcttacatcaatgaagtactttgtcaagattgga
 F V L W A H G F E L T S M K Y F V K I G
 cctgaaagaacgtgttgtctgtgtgacaaacgtgcaacttgcttttctacttcatcagat
 P E R T C C L C D K R A T C F S T S S D
 acttatgcctgctggaatcattctgtgggttttgactatgtctataaccatttatgatt
 T Y A C W N H S V G F D Y V Y N P F M I
 gatgttcagcagtggggctttacgggtaaccttcagagtaaccatgaccaacattgccag
 D V Q Q W G F T G N L Q S N H D Q H C Q
 gtacatggaaatgcacatgtggctagtgtgatgctatcatgactagatgttttagcagtc
 V H G N A H V A S C D A I M T R C L A V
 catgagtgctttgttaagcgcgttgattgggtctgttgaataccctattataggagatgaa
 H E C F V K R V D W S V E Y P I I G D E
 ctgagggttaattctgcttgcagaaaagtacaacacatgggttgtgaagtctgcattgctt
 L R V N S A C R K V Q H M V V K S A L L
 gctgataagtttccagtttcttcatgacataggaaatccaaaggctatcaagtgtgtgcct
 A D K F P V L H D I G N P K A I K C V P
 caggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttacaaa
 Q A E V E W K F Y D A Q P C S D K A Y K
 atagaggaactcttctattcttatgctatacatcacgataaattcactgatgggtgtttgt
 I E E L F Y S Y A I H H D K F T D G V C
 ttgttttgggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtgtaggtttgac
 L F W N C N V D R Y P A N A I V C R F D
 acaagagtcttgtcaaaacttgaacttaccagggtgtgatgggtgtagtttgtatgtgaat
 T R V L S N L N L P G C D G G S L Y V N
 aagcatgcattccacactccagcttttcgataaaaagtgcatttactaatttaaagcaattg
 K H A F H T P A F D K S A F T N L K Q L
 ccttttcttttactattctgatagtccttgtgagtcctcatggcaaacaagtagtgctcgat
 P F F Y Y S D S P C E S H G K Q V V S D

attgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtggtgct
I D Y V P L K S A T C I T R C N L G G A
gtttgcagacacccatgcaaatagagtaccgacagtacttggatgcatataatatgatgatt
V C R H H A N E Y R Q Y L D A Y N M M I
tctgctggatttagcctatggatttacaaacaatttgatacttataacctgtggaataca
S A G F S L W I Y K Q F D T Y N L W N T
tttaccaggttacagagttaa
F T R L Q S L

3'5' Frame 1

taaactctgtaacctggtaaattgtattccacagggttataagtatcaaattgtttgtaaatt
- T L - P G K C I P Q V I S I K L F V N
ccatagggttaaattccagcagaaatcatcatattatatgcatccaagtactgtcgggtactc
P - A K S S R N H H I I C I Q V L S V L
atttgcatgggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcaga
I C M V S A N S T T - I A S C N T R S R
tttgagtgggaacataatcaatatccgacactacttgtttgccatgagactcacaaggact
F E W N I I N I R H Y L F A M R L T R T
atcagaatagtaaaaagaaaggcaattgcttttaaattagtaaatgcactttttatcgaaagc
I R I V K E R Q L L - I S K C T F I E S
tggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagtt
W S V E C M L I H I Q T T T I T A W - V
caagtttgacaagactcttgtgtcaaacctacacacaattgcattgggtgggtaacgatc
Q V - Q D S C V K P T H N C I G W V T I
aacgtttacaattccaaaacaaacaaacaccatcagtgaatttatcgtgatgtatagcata
N V T I P K Q T N T I S E F I V M Y S I
agaatagaagagttcctctattttgtaagctttgtcactacatgggtgagcatcgtagaa
R I E E F L Y F V S F V T T W L S I V E
cttccattctacttcagcctgaggcacacacttgatagcctttggatttcctatgtcatg
L P F Y F S L R H T L D S L W I S Y V M
aagaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgttggtacttttct
K N W K L I S K Q C R L H N H V L Y F S
gcaagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaac
A S R I N P Q F I S Y N R V F N R P I N
gcgcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacaaactagc
A L N K A L M D C - T S S H D S I T T S
cacatgtgcatttccatgtacctggcaatgttggtcatgggttactctgaagggttaccgt
H M C I S M Y L A M L V M V T L K V T R
aaagccccactgctgaacatcaatcataaattgggttatagacatagtcaaaaccacaga
K A P L L N I N H K W V I D I V K T H R
atgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcaca
M I P A G I S I - - S R K A S C T F V T
cagacaacacgttcttttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaa
Q T T R S F R S N L D K V L H - C K L K
gccatgcgccccaaaggacgaacacgactctgtctgacaatcctttcagtgtatcactgag
A M R P K D E H D S V - Q S F Q C I T E
catttgtactatcttaatacgcactacattccaggggcaagcctttatacatgagtggtat
H L Y Y L N T H Y I P G Q A F I H E W Y
aagatgttttaaactgggtcacctgggtggagggttttgcattaactctgggtgaattctgtgtt

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K M F K L V T W W R F C I N S G E F C V
attttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcc
I F S V N I T S R Y S Y - V N T C R K S
tagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatc
- L E R - V S T H S I S S C M T A L Y I
aaagccaatccacgcacgaacgtgacgaatagcttcttcgcggtgataaacatattagg
K A N P R T N V T N S F F A G D K H I R
gtaaccattgacttggttaattcattttgaaacccatcatagagatgagtgctacggtaggt
V T I D L V I H F E T H H R D E S T V G
catgtccttttgggtatgcctagg
H V L W V C L

3'5' Frame 2

taaactctgtaacctggtaaatgtattccacaggttataagtatcaaattgtttgtaaattc
K L C N L V N V F H R L - V S N C L - I
cataggctaaatccagcagaaatcatcatattatatgcatccaagtactgtcgggtactca
H R L N P A E I I I L Y A S K Y C R Y S
tttgcattggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagat
F A W C L Q T A P P K L H R V I H V A D
ttgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggacta
L S G T - S I S D T T C L P - D S Q G L
tcagaatagtaaaagaaaggcaattgcttttaaattagtaaattgcactttttatcgaaagct
S E - - K K G N C F K L V N A L L S K A
ggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagttc
G V W N A C L F T Y K L P P S Q P G K F
aagtttgacaagactcttgtgtcaaacctacacacaattgcattgggtgggtaacgatca
K F D K T L V S N L H T I A L A G - R S
acgttacaattccaaaacaaacaaacaccatcagtgaaatttatcgtgatgtatagcataa
T L Q F Q N K Q T P S V N L S - C I A -
gaatagaagagttcctctattttgtaagctttgtcactacatggctgagcatcgtagaac
E - K S S S I L - A L S L H G - A S - N
ttccattctacttcagcctgaggcacacacttgatagccttttgatttcctatgtcatga
F H S T S A - G T H L I A F G F P M S -
agaactggaaacttatcagcaagcaatgcagacttcacaacccatgtgttgacttttctg
R T G N L S A S N A D F T T M C C T F L
caagcagaattaaccctcagttcatctcctataataggggtattcaacagaccaatcaacg
Q A E L T L S S S P I I G Y S T D Q S T
cgcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacactagcc
R L T K H S W T A K H L V M I A S Q L A
acatgtgcattttccatgtacctggcaatgtttgggtcatgggttactctgaagggttaccgta
T C A F P C T W Q C W S W L L - R L P V
aagccccactgctgaacatcaatcataaatgggttatagacatagtcaaaacccacagaa
K P H C - T S I I N G L - T - S K P T E
tgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacac
- F Q Q A - V S D E V E K Q V A R L S H
agacaacacgtttctttcaggtccaatcttgacaaagttacttcattgatgtaagctcaaag
R Q H V L S G P I L T K Y F I D V S S K
ccatgcgccccaaaggacgaacacgactctgtctgacaatccttttcagtgatcactgagc
P C A Q R T N T T L S D N P F S V S L S

atttgtactatcttaatacgcactacattccagggcaagcctttatacatgagtgggtata
 I C T I L I R T T F Q G K P L Y M S G I
 agatgttttaactgggtcacctgggtggaggttttgcattaactctgggtgaattctgtgtta
 R C L N W S P G G G F A L T L V N S V L
 ttttcagtggtcaacataaccagtcggtacagctactaagttaaacacctgtagaaaatcct
 F S V S T - P V G T A T K L T P V E N P
 agctggagaggttaggttagtaccacacagcatctctagttgcatgacagccctctacatca
 S W R G R L V P T A S L V A - Q P S T S
 aagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattaggg
 K P I H A R T - R I A S S R V I N I L G
 taaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggtaggtc
 - P L T W - F I L K P I I E M S L R - V
 atgtcctttgggtatgcctagg
 M S F G Y A -

3'5' Frame 3

taaactctgtaacctggtaaatgtattccacaggttataagtatcaaattgtttgtaaattcc
 N S V T W - M Y S T G Y K Y Q I V C K S
 ataggctaaatccagcagaaatcatcatattatatgcatccaagtactgtcgggtactcat
 I G - I Q Q K S S Y Y M H P S T V G T H
 ttgcatgggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagatt
 L H G V C K Q H H L N C I V - Y T - Q I
 tgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggactat
 - V E H N Q Y P T L L V C H E T H K D Y
 cagaatagtaaaaagaaaggcaattgcttttaaattagtaaatgcactttttatcgaaagctg
 Q N S K R K A I A L N - - M H F Y R K L
 gagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagttca
 E C G M H A Y S H T N Y H H H S L V S S
 agtttgacaagactccttgtgtcaaacctacacacaattgcattgggtgggtaacgatcaa
 S L T R L L C Q T Y T Q L H W L G N D Q
 cgttacaattccaaaacaaacaaacaccatcagtggaatttatcgtgatgtatagcataag
 R Y N S K T N K H H Q - I Y R D V - H K
 aatagaagagttcctctattttgtaagctttgtcactacatgggtgagcatcgtagaact
 N R R V P L F C K L C H Y M A E H R R T
 tccattctacttcagcctgaggcacacacttgatagcctttggatttcctatgtcatgaa
 S I L L Q P E A H T - - P L D F L C H E
 gaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgtttgtacttttctgc
 E L E T Y Q Q A M Q T S Q P C V V L F C
 aagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaacgc
 K Q N - P S V H L L - - G I Q Q T N Q R
 gcttaacaaagcactcatggactgctaacaatctagtcgatagcatcacaactagcca
 A - Q S T H G L L N I - S - - H H N - P
 catgtgcatttccatgtacctggcaatgttgggtcatggttactctgaaggttaccctgtaa
 H V H F H V P G N V G H G Y S E G Y P -
 agccccactgctgaacatcaatcataaatggggttatagacatagtcaaaacccacagaat
 S P T A E H Q S - M G Y R H S Q N P Q N
 gattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacaca
 D S S R H K Y L M K - K S K L H V C H T
 gacaacacgttctttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaagc

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D N T F F Q V Q S - Q S T S L M - A Q S
catgcgccccaaaggacgaacacgactctgtctgacaatcctttcagtgtatcactgagca
H A P K G R T R L C L T I L S V Y H - A
tttgtactatcttaatacgcactacattccaggggaagcctttatacatgagtggtataa
F V L S - Y A L H S R A S L Y T - V V -
gatgttttaaactgggtcacctgggtggagggttttgcattaactctgggtgaattctgtgttat
D V - T G H L V E V L H - L W - I L C Y
tttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatccta
F Q C Q H N Q S V Q L L S - H L - K I L
gctggagaggtagggttagtacccacagcatctctagttgcatgacagccctctacatcaa
A G E V G - Y P Q H L - L H D S P L H Q
agccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattagggt
S Q S T H E R D E - L L R G - - T Y - G
aaccattgacttggttaattcatttttgaaacccatcatagagatgagtctacggtaggtca
N H - L G N S F - N P S - R - V Y G R S
tgtcctttgggtatgcctagg
C P L G M P R

FIGURE 123

CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGT
.....i.....N..N.....i.....N....
TACCCTAATATGTTTATCACCCGCGAAGAAGCTATTTCGTACCGTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCA
.....i.....N.....N
TGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA
.....N.....
CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACAT
.....N.....N.....
CTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCAGTGATACACTGAA
.....N.....N.....N.....
AGGATTGTCAGACAGAGTCGTGTTTCGTCTTTGGGCGCATGGCTTTGAGCTTACATCAATGAAGTACTTTGTCAAGATTG
.....N.....N.....
GACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAAT
.....N.....
CATTCTGTGGGTTTTGACTATGTCTATAACCCATTTATGATTGATGTTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAG
.....N.....N.....N.....
TAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAG
.....N.....N.....N.....N.....i.....N.....
TCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGTTGAATACCTATTATAGGAGATGAAC TGAGGGTTAATTCTGCT
..N.....N.....
TGCAGAAAAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCCTTCATGACATAGGAAATCC
.....i.....N.....
AAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGACAAAGCTTACA
.....N.....N.....N.....
AAATAGAGGAACTCTTCTATTCTTATGCTATACATCACGATAAATTCAGTATGGTGTGTTTGTGTTTGGGAATTGTAAC
.....N.....N.....
GTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACCTTGAACCTACCAGGCTGTGA
.....N.....N.....
TGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAAT
.....N.....N.....
TGCCTTTCTTTTACTATTCTGATAGTCCTTGTGAGTCTCATGGCAAACAAGTAGTGTCCGATATTGATTATGTTCCACTC
.....i.....N.....
AAATCTGCTACGTGTATTACACGATGCAATTTAGGTGGTGTGTTTGCAGACACCATGCAATGAGTACCGACAGTACTT
.....N.....N.....N.....
GGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATA
..N.....N..N.....N.....
CATTTACCAGGTTACAGAGTTTA **SEQ ID NO: 10084**
.....

FIGURE 123 (contd.)

Pos	Score	Pred
21	0.651	Yes
45	0.354	-
48	0.387	-
60	0.590	Yes
76	0.470	-
90	0.676	Yes
145	0.192	-
160	0.410	-
172	0.290	-
247	0.221	-
286	0.219	-
333	0.373	-
355	0.178	-
381	0.286	-
439	0.405	-
459	0.204	-
547	0.289	-
580	0.447	-
597	0.449	-
604	0.290	-
646	0.427	-
667	0.427	-
673	0.208	-
679	0.317	-
694	0.180	-
702	0.554	Yes
710	0.151	-
724	0.384	-
778	0.151	-
819	0.711	Yes
865	0.306	-
917	0.230	-
931	0.214	-
941	0.190	-
985	0.274	-
1012	0.368	-
1060	0.206	-
1120	0.193	-
1135	0.185	-
1147	0.431	-
1240	0.562	Yes
1270	0.377	-
1304	0.190	-
1336	0.353	-
1342	0.312	-
1363	0.213	-
1374	0.178	-
1377	0.096	-
1400	0.056	-

FIGURE 124

Sequences:			(bits)	Value
gi	74827 pir	VFIHJH genome polyprotein 1b - murine hepatit...	638	0.0
gi	14917044 sp P29982 RRPB_CVMJH	RNA-directed RNA polymeras...	637	0.0
gi	26007546 ref NP_068668.2	ORF1ab polyprotein [Murine hep...	637	0.0
gi	7769342 gb AAF69332.1 AF208066_2	RNA-directed RNA polyme...	637	0.0
gi	6625761 gb AAF19384.1 AF201929_2	RNA-directed RNA polyme...	637	0.0
gi	2641128 gb AAB86818.1	RNA-directed RNA polymerase [muri...	635	0.0
gi	4377413 emb CAA36202.1	open reading frame 1b (AA 1-2733...	634	0.0
gi	133592 sp P16342 RRPB_CVMA5	RNA-DIRECTED RNA POLYMERASE ...	634	0.0
gi	26008080 ref NP_150073.2	orflab polyprotein [Bovine cor...	633	e-180
gi	15077820 gb AAK83365.1	replicase [bovine coronavirus]	633	e-180
gi	18033972 gb AAL57305.1	replicase [bovine coronavirus]	633	e-180
gi	7769353 gb AAF69342.1 AF208067_2	RNA-directed RNA polyme...	633	e-180
gi	17529672 gb AAL40397.1 AF220295_2	RNA polymerase 1b [bov...	623	e-177
gi	25121571 ref NP_740618.1	coronavirus nsp11 [Murine hepa...	622	e-177
gi	26008092 ref NP_742140.1	coronavirus nsp11 [Bovine coro...	617	e-175
gi	10242469 ref NP_066134.1	ORF1ab polyprotein; frameshift...	575	e-163
gi	14149033 emb CAC39112.1	replicase polyprotein 1ab [Avia...	575	e-163
gi	458735 emb CAA83018.1	potential chimeric protein [Avian...	570	e-161
gi	133594 sp P26314 RRPB_IBVB	RNA-DIRECTED RNA POLYMERASE (...)	570	e-161
gi	29293454 gb AAO67706.1	ORF1b polyprotein [Avian infecti...	565	e-160
gi	25121555 ref NP_740631.1	coronavirus nsp11 [Avian infec...	559	e-158
gi	9635157 ref NP_058422.1	replicase [Transmissible gastro...	545	e-153
gi	19387582 ref NP_598309.1	Pol1 [porcine epidemic diarrhe...	541	e-152
gi	12175747 ref NP_073549.1	replicase polyprotein 1ab [Hum...	535	e-151
gi	133591 sp P18458 RRPB_BEV	RNA-directed RNA polymerase (O...	50	8e-05
gi	1513061 dbj BAA13323.1	cyanoprotein alpha subunit precu...	35	3.7

Alignments

>gi|74827|pir|VFIHJH genome polyprotein 1b - murine hepatitis virus
(strain JHM)

Length = 2731

Score = 638 bits (1645), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGNTNLPQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHATRDSIGTNFPLQ 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ 1704

Query: 126 MLSDTLKGLSDRVVFLVLAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCSVCNKRATCFNSRTGYGWCWR 1764

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1765 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 1824

157/193

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAICVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVLS
Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLSK 1939

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 1940 LNLPGCNGGSLYVNKHAFHTNPFTRAFAFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 1999

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 2000 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2059

Query: 486 L 486
L
Sbjct: 2060 L 2060

>gi|14917044|sp|P29982|RRPB_CVMJH RNA-directed RNA polymerase (ORF1B)
gi|7583321|gb|AAA46458.2| open reading frame 1b [murine hepatitis virus]
Length = 2731

Score = 637 bits (1644), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHATRDSIGTNFPLQ 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ
Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLVPLMSRQKQWDVVRIRIVQ 1704

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW
Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVCSVCNKRATCFNSRTGYGWCWR 1764

Query: 186 HSVGFDYVYNPFMIDVQWQGTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
Sbjct: 1765 HSYSCDYLYNPLIVDIQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 1824

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAICVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVLS
Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLSK 1939

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 1940 LNLPGCNGGSLYVNKHAFHTNPFTRAFAFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 1999

158/193

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 2000 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2059

Query: 486 L 486
L
Sbjct: 2060 L 2060

>gi|26007546|ref|NP_068668.2| ORFlab polyprotein [Murine hepatitis virus]
Length = 7178

Score = 637 bits (1644), Expect = 0.0
Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
Sbjct: 6032 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFD AEGAHAIRDSIGTNFPLQ 6091

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
Sbjct: 6092 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 6151

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
Sbjct: 6152 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYYGCWR 6211

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
Sbjct: 6212 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 6271

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
Sbjct: 6272 SVNWNLEYPIISNEVSVNTSCLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 6329

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVDPANA+VCRFDTRVL+
Sbjct: 6330 KFYDASPV---VKS VKQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 6386

Query: 366 LNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVPL 425
LNLPGC+GGSLYVnKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
Sbjct: 6387 LNLPGCNGGSlyVnKHAFHTSPFTRAAFENLKMPFPFFYYSDTPCVYMEGMESKQVDYVPL 6446

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
Sbjct: 6447 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 6506

Query: 486 L 486
L
Sbjct: 6507 L 6507

>gi|7769342|gb|AAF69332.1|AF208066_2 RNA-directed RNA polymerase [murine
hepatitis virus]
Length = 2732

Score = 637 bits (1644), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 1586 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFDAEGAHATRDSIGTNFPLQ 1645

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ
 Sbjct: 1646 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIIVQ 1705

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW
 Sbjct: 1706 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVKNKRATCFNSRTGYYGCWR 1765

Query: 186 HSVGFDYVYNPFMIDVQQWGF'TGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1766 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDLCVHKGAVASSDAIMTRCLAVHDCFCCK 1825

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
 V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1826 SVNWSLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1883

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVDPANA+VCRFDTRVL+
 Sbjct: 1884 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1940

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1941 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2000

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
 Sbjct: 2001 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2060

Query: 486 L 486
 L
 Sbjct: 2061 L 2061

>gi|6625761|gb|AAF19384.1|AF201929_2 RNA-directed RNA polymerase [murine hepatitis virus strain 2]

gi|7739595|gb|AAF68920.1|AF207902_2 RNA-directed RNA polymerase [murine hepatitis virus strain ML-11]

Length = 2733

Score = 637 bits (1643), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFDAEGAHATRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

160/193

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVCKNRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTNSHDLICSVHKGAVHASSDAIMTRCLAVHDCFCCK 1826

Query: 246 RVDWSVEYPIIGDELVRNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWSLEYPIISNEVSVNTSCRLQLQVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNS 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVDPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSGLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
LNLPGC+GGSGLYVKNHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSGLYVKNHAFHTSPFTRAFFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486
L

Sbjct: 2062 L 2062

>gi|2641128|gb|AAB86818.1| RNA-directed RNA polymerase [murine hepatitis virus]

Length = 2733

Score = 635 bits (1637), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIKDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTNSHDPICSVHKGAVHASSDAIMTRCLAVHDCFCCK 1826

Query: 246 RVDWSVEYPIIGDELVRNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

161/193

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486
 L

Sbjct: 2062 L 2062

>gi|4377413|emb|CAA36202.1| open reading frame 1b (AA 1-2733) [Murine hepatitis virus]
 Length = 2733

Score = 634 bits (1636), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGWCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

162/193

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486

L

Sbjct: 2062 L 2062

>gi|133592|sp|P16342|RRPB_CVMA5 RNA-DIRECTED RNA POLYMERASE (ORF1B)
gi|93916|pir|S15760 genome polyprotein - murine hepatitis virus (strain A59)

Length = 2733

Score = 634 bits (1636), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65

+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIRDSIGTNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQ 125

LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185

MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245

HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCK 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAICVPQAEVEW 305

V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365

KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425

LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRAFFENLKMPFFYYSDTPCVMEGMESKQVDYVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485

+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS 2061

Query: 486 L 486

L

Sbjct: 2062 L 2062

>gi|26008080|ref|NP_150073.2| orflab polyprotein [Bovine coronavirus]

Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAEGAHATRDSIGTNFPLQ 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYYGCWR 6127

Query: 186 HSVGFDDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
 Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 6187

Query: 246 RVDWSVEYPIIGDELRVNSACRQVQHMVKSALLADKFPVLHDIGNPKAIKCVPOAEVEW 305
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCDIGNPKAIACV--KDFDF 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVND+YP NA+VCRFDTRVL+N
 Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVNDKYPPNAVVCRFDTRVLNN 6302

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 6303 LNLPGCNGGSLYVNKHAFHTKPFSSRAAFEHLKMPFFYYSDTPCVYMDGMDAKQVDYVPL 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
 Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWYKTFDFYNLWNTFTKLQS 6422

Query: 486 L 486
 L
 Sbjct: 6423 L 6423

>gi|15077820|gb|AAK83365.1| replicase [bovine coronavirus]
 Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAEGAHATRDSIGTNFPLQ 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYYGCWR 6127

164/193

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAVASSDAIMTRCLAVYDCFCN 6187

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQH MVVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L YS+ H D F DG+C+FWNCNVDP+YP NA+VCRFDTRVL+N
Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAVVCRFDRVLNN 6302

Query: 366 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDYVPL 425
LNLPGC+GGS LYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
Sbjct: 6303 LNLPGCNGGS LYVNKHAFHTKPF SRAAFEHLKMPFFYYSDTPCVYMDGMDAKQVDYVPL 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS 6422

Query: 486 L 486
L
Sbjct: 6423 L 6423

>gi|18033972|gb|AAL57305.1| replicase [bovine coronavirus]
Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG TNLPLQ 65
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 5948 VTYSRLISLMGFKLDVTL DGYCKLFITKEEA VKRVRAWVGFD AEGA HATRDSIGTNFPLQ 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD TYACWN 185
M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYYGCWR 6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAVASSDAIMTRCLAVYDCFCN 6187

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQH MVVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L YS+ H D F DG+C+FWNCNVDP+YP NA+VCRFDTRVL+N
Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKYPNAVVCRFDRVLNN 6302

165/193

Query: 366 LNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDyVPL 425
 LNLPGC+GGSLyVnKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 6303 LNLPGCNGGSlyVnKHAFHTKPFsRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDyVPL 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDtYNLWNTfTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTfT+LQS
 Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTfTKLQS 6422

Query: 486 L 486
 L
 Sbjct: 6423 L 6423

>gi|7769353|gb|AAF69342.1|AF208067_2 RNA-directed RNA polymerase [murine hepatitis virus]
 Length = 2733

Score = 633 bits (1633), Expect = e-180

Identities = 285/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRawIGFDVEGCHATrDAVGtNLPLQ 65
 ++Y RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 1587 VSYRLISLMGFKLdLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGtNFPLQ 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENntEFTRVNAKPPPGDQFKHLIPLMYKGLPWNvVRIKIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKAARAPPGEQFKHLIPLMSRGQKWdVVRIRIVQ 1706

Query: 126 MLSDTLKGLSDRVVFVLWAHGfELTSMKYfVKIGPERTCCLCDKRATCFSTSSDtyACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 1707 MLSdHLVdLADSVVLVTWAASFELTCLRYfAKVGREvVCSVCTKRATCFNSRTGYYGCWR 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1767 HSYSCDyLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAHVASSDAIMTRCLAVHdCFCK 1826

Query: 246 RVDWSVEYPIIGDELrvNSACrkVQhMVVKSALLADKfPVLHDIGNPKAIKCVpQAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1827 SVNWNLEyPIISNEVSVNTScRLlQRVMfRAAMLCNRYdVCyDIGNPKGLACVKG--YDF 1884

Query: 306 KFYDAQPCSDKAYKIEELfYSYAIHhDKFTDgVCLfWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+fWNCNVd+YPANA+vCRFDTRVL+
 Sbjct: 1885 KFYDASPv---VKSvKQfVYKYEAHKDQFLDGLCMfWNCNVdKYPANAVvCRFDTRVLNK 1941

Query: 366 LNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDyVPL 425
 LNLPGC+GGSLyVnKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1942 LNLPGCNGGSlyVnKHAFHTSPfTRAAfENLKPMPPFFYYSDTPCVYMEGMESKQVDyVPL 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDtYNLWNTfTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTfT+LQS
 Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTfTRLQS 2061

Query: 486 L 486
 L
 Sbjct: 2062 L 2062

166/193

>gi|17529672|gb|AAL40397.1|AF220295_2 RNA polymerase 1b [bovine coronavirus]

Length = 2685

Score = 623 bits (1607), Expect = e-177

Identities = 282/481 (58%), Positives = 365/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
Sbjct: 1574 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAGEAHATRDSIGTNFPLQ 1633

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQ 125
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
Sbjct: 1634 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 1693

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
M +D L LSD VV V WA FELT ++YF K+G E +C + KRAT +++ + Y CW
Sbjct: 1694 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVSTKRATAYNSRTGYYGCWR 1753

Query: 186 HSVGFDYVYNPFMIDVQQWGF TGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
Sbjct: 1754 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 1813

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
Sbjct: 1814 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 1871

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L Y + H D F DG+C+FWNCNVDP+YP NA+VCRFDTRVL+N
Sbjct: 1872 KFYDAQPI---VKSVKTLLEYFFEAHKDSFKDGLCMFWNCNVDPKYPNAVVCRFDTRVLNN 1928

Query: 366 LNLPGCDGGSlyVnkhafHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVPL 425
LNLPGC+GGSlyVnkhafHT F ++AF +LK +PFFYYSD+PC +DYVPL
Sbjct: 1929 LNLPGCNGGSlyVnkhafHTKPFsRAAFehLkPMPFFYYSDTPCVYMDGMDAKQVDYVPL 1988

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
Sbjct: 1989 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS 2048

Query: 486 L 486
L
Sbjct: 2049 L 2049

>gi|25121571|ref|NP_740618.1| coronavirus nsp11 [Murine hepatitis virus]
Length = 521

Score = 622 bits (1603), Expect = e-177

Identities = 284/479 (59%), Positives = 362/479 (75%), Gaps = 5/479 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
Sbjct: 48 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGEAHAIKRD SIGTNFPLQ 107

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQ 125

167/193

LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 108 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 167
 Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 168 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGGYGCWR 227
 Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 228 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 287
 Query: 246 RVDWSVEYPIIGDELVRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 288 SVNWNLEYPIISNEVSVNTSCRLLQVRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 345
 Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNS 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+
 Sbjct: 346 KFYDASPV---VKS VKQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVCRFDTRVLNK 402
 Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 403 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKPMFPFFYYSDTPCVMEGMESKQVDYVPL 462
 Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQ 484
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQ
 Sbjct: 463 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQ 521

>gi|26008092|ref|NP_742140.1| coronavirus nsp11 [Bovine coronavirus]
 Length = 521

Score = 617 bits (1590), Expect = e-175

Identities = 282/479 (58%), Positives = 365/479 (76%), Gaps = 5/479 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 48 VTYSRLISLMGFKLDVTLTDGYCKLFTITKEEAVKRVRRAWVGFDAEGAHA TRDSIGTNFPLQ 107
 Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 108 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 167
 Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 168 MFADHLIDLSDCVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGGYGCWR 227
 Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
 Sbjct: 228 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 287
 Query: 246 RVDWSVEYPIIGDELVRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 288 NINWNVEYPIISNELSINTSCRVLQVRMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 345
 Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNS 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N

168/193

Sbjct: 346 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNV DKYPPNAVVC RFDT RVLNN 402

Query: 366 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425
LNLPGC+GGS LYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL

Sbjct: 403 LNLPGCNGGS LYVNKHAFHTKPF SRAAFEHLKPM PFFYYSDTPCVYMDGMDAKQVDYVPL 462

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQ

Sbjct: 463 KSATCITRCNLGGAVCLKHAE EYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQ 521

>gi|10242469|ref|NP_066134.1| ORFlab polyprotein; frameshift product [Avian
infectious bronchitis
virus]
Length = 6629

Score = 575 bits (1482), Expect = e-163

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG TNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP

Sbjct: 5515 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIG TNLPL 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNV VRIKIV 124
Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV

Sbjct: 5575 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFSAKPWHVIRPRIV 5634

Query: 125 QMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD TYACW 184
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW

Sbjct: 5635 QMLADNLCNVSDCVFVVTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGF TGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F

Sbjct: 5694 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVK SALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V

Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMYNACVDALKVNVVYDIGNPKGIKCVRRGDVN 5813

Query: 305 WKFYDAQPCSDKAYKIEELFY SYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNV D YP N++VCR+DTR LS

Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNLVCRYDTRNLS 5870

Query: 365 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYV 424
NLPGC+GGS LYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V

Sbjct: 5871 VFNLPGCNGGS LYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ

Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAV TAGFTFWVTNKLNPYNLWKSFSALQ 5989

Query: 485 SL 486

S+

Sbjct: 5990 SI 5991

169/193

>gi|14149033|emb|CAC39112.1| replicase polyprotein lab [Avian infectious
bronchitis virus (strain
Beaudette CK)]
Length = 6629

Score = 575 bits (1482), Expect = e-163

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 5515 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPLF 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIV 124
Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
Sbjct: 5575 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 5634

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
QML+D L +SD VVFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
Sbjct: 5635 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F
Sbjct: 5694 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASVDAIMTRCLAINNAFC 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAIKCVPQAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN 5813

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNV D YP N++VCR+DTR LS
Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 5870

Query: 365 NLNLPGCDGGSlyVnkhafHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVP 424
NLPGC+GGSlyVnkhaf+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 5871 VFNLPGCNGGSlyVnkhafYTPKFDRI SFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 5989

Query: 485 SL 486
S+
Sbjct: 5990 SI 5991

>gi|458735|emb|CAA83018.1| potential chimeric protein [Avian infectious
bronchitis virus]
Length = 2155

Score = 570 bits (1470), Expect = e-161

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 1596 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPLF 1655

170/193

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 1656 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 1715

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 1716 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 1774

Query: 185 NHSVGFVDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DAIMTRCLA++ F
 Sbjct: 1775 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC 1834

Query: 245 KRVDWSVEYPIIGDELVRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
 Sbjct: 1835 QDVNWDLTYPHIANEDEVNSSCRYLQRMYNACVDALKVNVVDIGNPKGIKCVRRGDVN 1894

Query: 305 WKFYDAQPCSDKAYKIEELFYSYAIHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
 ++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
 Sbjct: 1895 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 1951

Query: 365 NLNLPGLCDGGSILYVKNHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVP 424
 NLPGL+GGSLYVKNHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
 Sbjct: 1952 VFNLPGLCNGGSILYVKNHAFYTPKFDRIISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 2010

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
 Sbjct: 2011 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 2070

Query: 485 SL 486
 S+
 Sbjct: 2071 SI 2072

>gi|133594|sp|P26314|RRPB_IBVB RNA-DIRECTED RNA POLYMERASE (ORF1B)
 gi|74826|pir||VFIHB2 genome polyprotein - avian infectious bronchitis
 virus (strain
 Beaudette)
 gi|292953|gb|AAA70234.1| pol protein [Avian infectious bronchitis virus]
 gi|331173|gb|AAA46224.1| ORF1b [Avian infectious bronchitis virus]
 Length = 2652

Score = 570 bits (1469), Expect = e-161

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
 Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDEATHACGTNIGTNLPL 1597

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 1598 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 1657

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 1658 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 1716

171/193

Query: 185 NHSVGFDDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F
Sbjct: 1717 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASVDAIMTRCLAINNAFC 1776

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 1777 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN 1836

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
Sbjct: 1837 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 1893

Query: 365 NLNLPGLCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVP 424
NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 1894 VFNLPGCNGGSLYVNKHAFYTPKFDRISEFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 1952

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
Sbjct: 1953 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 2012

Query: 485 SL 486
S+
Sbjct: 2013 SI 2014

>gi|29293454|gb|AAO67706.1| ORF1b polyprotein [Avian infectious bronchitis virus]

Length = 2649

Score = 565 bits (1455), Expect = e-160

Identities = 261/482 (54%), Positives = 342/482 (70%), Gaps = 8/482 (1%)

Query: 5 DMTYRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLPL
Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFVDVEATHACGTNIGTNLPL 1597

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIV 124
Q+GFSTG + V P G +DT F VN+K PPG+QF HL L PW+V+R +IV
Sbjct: 1598 QVGFSTGADFVVTPEGLIDTSIGNNFEPVNSKAPPGEQFNHLRALFKSAKPWHVIRPRIV 1657

Query: 125 QMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
Sbjct: 1658 QMLADNLCNVSDCVFVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 1716

Query: 185 NHSVGFDDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +G VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DA+MTRCLA++ F
Sbjct: 1717 RHCLG---VYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASADAVMTRCLAINNAFC 1773

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304
K V+W ++YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 1774 KDVNWELQYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN 1833

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y+ H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
Sbjct: 1834 FRFYDKNPIVNVKQFE---YDYSQHKDKFADGLCMFWNCNVDCYPENSLVCRYDTRNLS 1890

172/193

Query: 365 NLNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVP 424
NLPGC+GGSlyVnKHAFHTP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 1891 VFNLPGCNGGSlyVnKHAFHTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 1949

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ F+ YNLW F+ LQ
Sbjct: 1950 LATKDCITKCNIGGAVCKKHAQMYAEFVFSYNAAVTAGFTFWVTNNFNPYNLWKNFSALQ 2009

Query: 485 SL 486
S+
Sbjct: 2010 SI 2011

>gi|25121555|ref|NP_740631.1| coronavirus nsp11 [Avian infectious
bronchitis virus]
Length = 521

Score = 559 bits (1440), Expect = e-158
Identities = 261/480 (54%), Positives = 342/480 (71%), Gaps = 5/480 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
Sbjct: 47 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPF 106

Query: 65 QLGfSTGVNLVAVPTGYVDTEENTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIV 124
Q+GfSTG+ V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
Sbjct: 107 QVGfSTGADfVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 166

Query: 125 QMLSDTLKGLSDRVFVLWAHGfELTSMKYFVKIGPERTCCLCDKRATCFSTSSDtyACW 184
QML+D L +SD VVfV W HG ELT+++YfVKIG E+ C C RAT F++ + YACW
Sbjct: 167 QMLADNLCNVSDCVFVTWCHGLELTTLRYfVKIGKEQVCS-CGSRATTFNSHTQAYACW 225

Query: 185 NHSVGfDYVYNPFMIDVQQWGTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GfD+VYNP ++D+QQWG++GNLQ NHD HC VHg+AHVAS DAIMTRCLA++ F
Sbjct: 226 KHCLGfDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAHVASVDAIMTRCLAINNAFC 285

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
Sbjct: 286 QDVNWDLTYPHIANEDEVNSSCRYLQRMylNACVDALKVNVVYDIGNPKGIKCVRRGDVN 345

Query: 305 WKfYDAQPCSDKAYKIEELfYSYAIHHDKfTDGVCLFWNCNVDRYPANAIVCRfDTRVLS 364
++fYD P + E Y Y H DKF DG+C+fWNCNVd YP N++VCR+DTR LS
Sbjct: 346 FRfYDKNPfIVRNvkQfE---YDYNQHkDKfADGLCMfWNCNVdCYPDNSLVCRYDTRNLS 402

Query: 365 NLNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSdIDYVP 424
NLPGC+GGSlyVnKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
Sbjct: 403 VFNLPGCNGGSlyVnKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 461

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
Sbjct: 462 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 521

>gi|9635157|ref|NP_058422.1| replicase [Transmissible gastroenteritis
virus]
gi|7801348|emb|CAB91143.1| replicase [Transmissible gastroenteritis virus]

173/193

Length = 6685

Score = 545 bits (1403), Expect = e-153

Identities = 261/484 (53%), Positives = 335/484 (69%), Gaps = 13/484 (2%)

Query: 4 KDMTYRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP 63
 KD+ Y +IS MGF+ + GY +F TR+ A+R+VRAW+GFDVEG H D VGTN+P
 Sbjct: 5574 KDVKYANVISYMGFRFEANIPGYHTLFCTRDFAMRNVRAWLGFDVEGAHVCGDNVGTNP 5633

Query: 64 LQLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKI 123
 LQLGFS GV+ V G V TE V A+ PPG+QF HLIPLM KG PW++VR +I
 Sbjct: 5634 LQLGFSNGVDFVQTEGCVITEKGNSEVVKARAPPGEQFAHLIPLMRKGQPHIVRRRI 5693

Query: 124 VQMLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIG-PERTCCLCDKRATCFSTSSDTYA 182
 VQM+ D GLSD ++FVLWA G ELT+M+YFVKIG P++ C C K ATC+S+S YA
 Sbjct: 5694 VQMVCDYFDGLSDILIFVLWAGGLELTMMRYFVKIGRPQK--CECGKSATCYSSSQSVYA 5751

Query: 183 CWNHSGVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHEC 242
 C+ H++G DY+YNP+ ID+QQWG+TG+L NH + C +H N HVAS DAIMTRCLA+H+C
 Sbjct: 5752 CFKHALGCDYLYNPYCIDIQQWGYTGSLSMNHHEVCNIHRNEHVASGDAIMTRCLAIHDC 5811

Query: 243 FVKRVDWSVEYPIIGDELRVNSACRKVQHMMVKSALLADKFPVLHDIGNPKAIKCVPAE 302
 FVKRVDWS+ YP I +E ++N A R VQ V+K+AL +HD+GNPK I+C
 Sbjct: 5812 FVKRVDWSIVYPFIDNEEKINKAGRIVQSHVMKAALKIFNPAAIHDVGNPKGIRCA-TTP 5870

Query: 303 VEWKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRV 362
 + W YD P ++ + L Y Y +H +G+ LEWNCNVDP YP +IVCRFDTR
 Sbjct: 5871 IPWFCYDRDPINN---NVRCLDYDYMVHGQ--MNLMLFWNCNVDMYPEFSIVCRFDTRT 5925

Query: 363 LSNLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDY 422
 S L+L GC+GG+LYVN HAFHTPA+D+ AF LK +PFFYY DS CE V +Y
 Sbjct: 5926 RSKLSLEGCGNGALYVNNHAFHTPAYDRRAFAKLKMPFFYYDDSNC-----LVDGQPNY 5981

Query: 423 VPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTR 482
 VPLKS CIT+CN+GGAVC+ HA YR Y++ YN+ + AGF++W + FDTY LW+ F
 Sbjct: 5982 VPLKSNVCITKCNIGGAVCKKHAALYRAYVEDYNIFMQAGFTIWCQNFDTYMLWHGFVN 6041

Query: 483 LQSL 486
 ++L
 Sbjct: 6042 SKAL 6045

>gi|19387582|ref|NP_598309.1| Pol1 [porcine epidemic diarrhea virus]

gi|13752450|gb|AAK38661.1| Pol1 [porcine epidemic diarrhea virus]

Length = 6781

Score = 541 bits (1394), Expect = e-152

Identities = 256/480 (53%), Positives = 334/480 (69%), Gaps = 12/480 (2%)

Query: 8 YRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLG 67
 Y +IS MGF+ + + + +F TR+ A+R+VR W+GFDVEG H VGTN+PLQLG
 Sbjct: 5675 YEHVISFMGFRFDINIPNHHTLFCTRDFAMRNVRGWLGFDVEGAHVVGSNVGTNPVPLQLG 5734

Query: 68 FSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQML 127
 FS GV+ V P G V TE+ V A+ PPG+QF HL+PL+ +G PW+VVR +IVQM
 Sbjct: 5735 FSNVDFVVRPEGCVVTESGDYIKPVRARAPPGEQFAHLLPLLKRGQPDVVRKRIVQMC 5794

Query: 128 SDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNHS 187
SD L LSD ++FVLWA G ELT+M+YFVKIGP ++C C K ATC++++ TY C+ H+
Sbjct: 5795 SDYLANLSDILIFVLWAGGLELTTMRYFVKIGPSKSCD-CGKVATCYNALHTYCCFKHA 5853

Query: 188 VGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDALMTRCLAVHECFVKRV 247
+G DY+YNP+ ID+QQWG+ G+L NH +HC VH N HVAS DAIMTRCLA+H+CFVK V
Sbjct: 5854 LGCDYLYNPYCIDIQWGYKGSLSLNHHEHCNVHRNEHVASGDAIMTRCLAIHDCFVKNV 5913

Query: 248 DWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEWKF 307
DWS+ YP IG+E +N + R VQ ++S L ++DIGNPK I+C + +W
Sbjct: 5914 DWSITYPFIGNEAVINKSGRIVQSHTRMSVLKLYNPKAIYDIGNPKGIRCA-VTDAKWFC 5972

Query: 308 YDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNLN 367
+D P + +E Y Y I H +F DG+CLFWNCNVD YP ++VCRFDTR S LN
Sbjct: 5973 FDKNPTNSNVKTL---YDY-ITHGQF-DGLCLFWNCNVDMPYEFSSVCRFDTRCRSPLN 6027

Query: 368 LPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPLKS 427
L GC+GGSLYVN HAFHTPAFDK AF LK +PFF+Y D+ C+ ++ I+YVPL++
Sbjct: 6028 LEGCNGGSLYVNNHAFHTPAFDKRAFAKLKMPFFFYDDTECD----KLQDSINYVPLRA 6083

Query: 428 ATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFT-RLQSL 486
+ CIT+CN+GGAVC H Y Y++AYN SAGF++W+ FDTYNLW TF+ LQ L
Sbjct: 6084 SNCITKCNVGGAVCSKHCAMYHSYVNAYNTFTSAGFTIWWPTSFDTYNLWQTFSSNNLQGL 6143

>gi|12175747|ref|NP_073549.1| replicase polyprotein lab [Human coronavirus 229E]

gi|12082740|gb|AAG48591.1|AF304460_2 replicase polyprotein lab [Human coronavirus 229E]

Length = 6758

Score = 535 bits (1379), Expect = e-151

Identities = 254/478 (53%), Positives = 329/478 (68%), Gaps = 13/478 (2%)

Query: 7 TYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQL 66
TY +IS MGF+ + + G ++F TR+ A+RHVR W+G DVEG H T D VGTN+PLQ+
Sbjct: 5642 TYEHVISYMGFRFDVSMPSHSLFCTRDFAMRHVRGWLGMDEGAHVTDGNVGTNVPLQV 5701

Query: 67 GFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVRIKIVQM 126
GFS GV+ VA P G V T + V A+ PPG+QF H++PL+ KG PW+V+R +IVQM
Sbjct: 5702 GFSNGVDFVAQPEGCVLTNTGSSVVKPVRARAPPGEQFTHIVPLLRKGQPSVLRKRIVQM 5761

Query: 127 LSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNH 186
++D L G SD +VFVLWA G ELT+M+YFVKIG + C C ATC+++ S+ Y C+ H
Sbjct: 5762 IADFLAGSSDVLVFLWAGGLELTTMRYFVKIGAVKH-CQCGTVATCYNVSNVNDYCCFKH 5820

Query: 187 SVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDALMTRCLAVHECFVKRV 246
++G DYVYNP++ID+QQWG+ G+L +NH C VH N HVAS DAIMTRCLAV++CFVK
Sbjct: 5821 ALGCDYVYNPYVIDIQWGYVGSLSLNHHAICNVHRNEHVASGDAIMTRCLAVYDCVKN 5880

Query: 247 VDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEWK 306
VDWS+ YP+I +E +N R VQ ++++A+ +HDIGNPK I+C + +W
Sbjct: 5881 VDWSITYPMIANENAINKGGRTVQSHIMRAAIKLYNPKAIHDIGNPKGIRCA-VTDAKWY 5939

Query: 307 FYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNL 366

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YD P + +E Y Y H DG+CLFWNCNVD YP +IVCRFDTR S L
Sbjct: 5940 CYDKNPINSNVKTLE---YDYMTHGQ--MDGLCLFWNCNVDMYPEFSIVCRFDTRTRSTL 5994

Query: 367 NLPGCDGGSGLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSD-IDYVPL 425
NL G +GGSGLYVN HAFHTPA+DK A LK PFFYY D CE VV D ++YVPL
Sbjct: 5995 NLEGVNGGSGLYVNNHAFHTPAYDKRAMAKLKPAPFFYYDDGSCE-----VVHDQVNYVPL 6049

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRL 483
++ CIT+CN+GGAVC HAN YR Y+++YN+ AGF++W+ FD YNLW TFT +
Sbjct: 6050 RATNCITKCNIGGAVCSKHANLYRAYVESYNIFTQAGFNIWVPTTFDCYNLWQTFTEV 6107

>gi|133591|sp|P18458|RRPB_BEV RNA-directed RNA polymerase (ORF1B)
gi|94017|pir||S11238 polymerase - Berne virus
gi|1334814|emb|CAA36601.1| 2nd polymerase reading frame (AA 1-2291) [Berne virus]

Length = 2291

Score = 50.1 bits (118), Expect = 8e-05

Identities = 37/103 (35%), Positives = 54/103 (52%), Gaps = 11/103 (10%)

Query: 140 FVLWAHGFELTSMKYFVKIGPERTC--CLCDKRATCFSTSSDTYACWNHSGVF--DYVYN 195
F+L++ +L S+K++V+ TC C C + A C + Y C N G + N
Sbjct: 1511 FILYSCSNLKSLLKFYVEFD---TCYFCSCGEMAICLMRDGN-YKCRNCYGGMLISKLVN 1566

Query: 196 PFMIDVQQWGFTGNLQSNHDQHC-QVHGNAHVASCDAIMTRCL 237
+DVQ+ LQ HD C Q HG++H A CDA+MT+CL
Sbjct: 1567 CKYLDVQKERV--KLQDAHDAICQQFHHGDSHEALCDAVMTKCL 1607

>gi|1513061|dbj|BAA13323.1| cyanoprotein alpha subunit precursor [Riptortus clavatus]

Length = 693

Score = 34.7 bits (78), Expect = 3.7

Identities = 16/36 (44%), Positives = 22/36 (61%), Gaps = 1/36 (2%)

Query: 371 CDGGSGLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSD 406
C G LY +KHA P FD+ A+ + Q+P FY+ D
Sbjct: 643 CGGSKLYDSKHAMGFP-FDRPAYPDAFQVPNFYFKD 677

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

Posted date: Apr 11, 2003 2:30 AM

Number of letters in database: 454,141,287

Number of sequences in database: 1,411,415

Lambda	K	H
0.325	0.139	0.456

Gapped

Lambda	K	H
0.267	0.0410	0.140

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Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 473,361,261
Number of Sequences: 1411415
Number of extensions: 20503315
Number of successful extensions: 51018
Number of sequences better than 10.0: 27
Number of HSP's better than 10.0 without gapping: 26
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 50937
Number of HSP's gapped (non-prelim): 33
length of query: 486
length of database: 454,141,287
effective HSP length: 127
effective length of query: 359
effective length of database: 274,891,582
effective search space: 98686077938
effective search space used: 98686077938
T: 11
A: 40
X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 75 (33.5 bits)

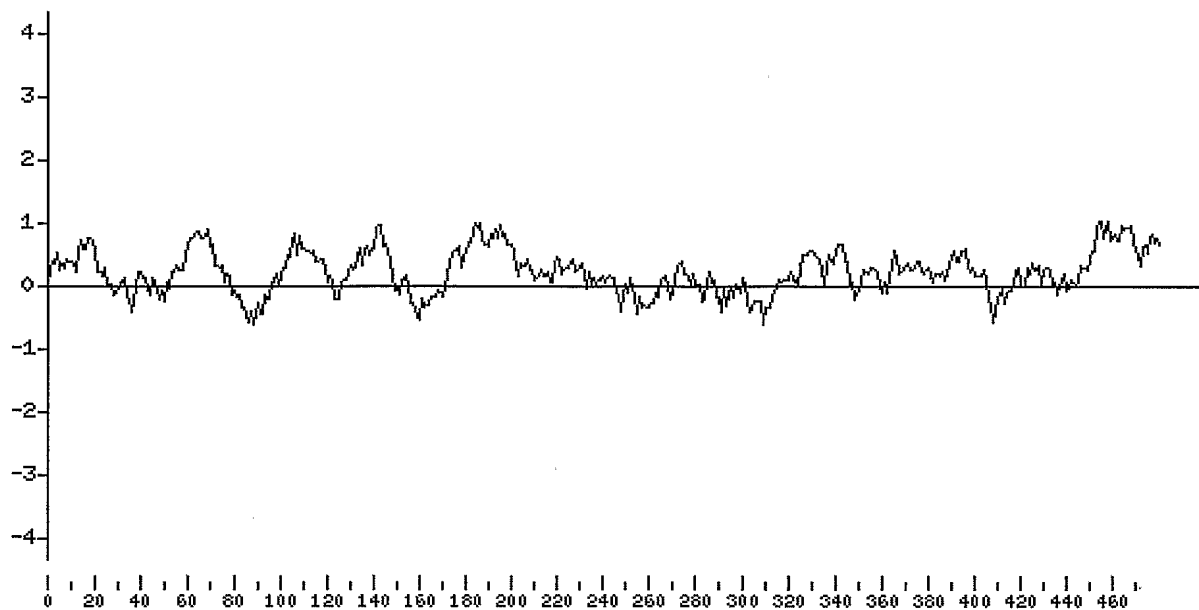
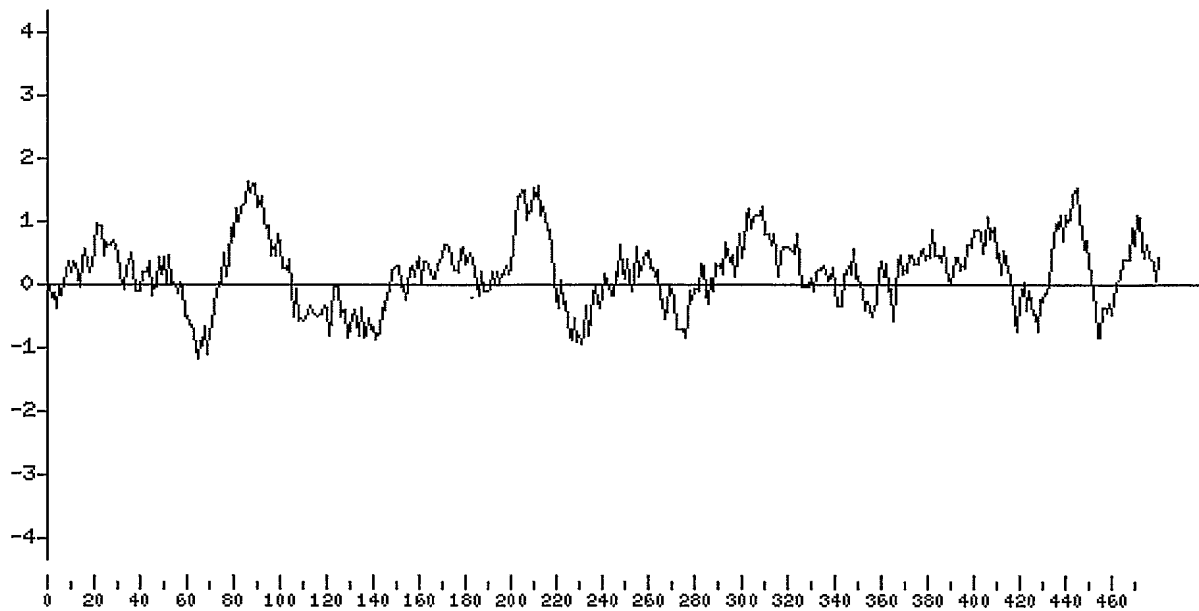
FIGURE 125**FIGURE 125A****FIGURE 125B**

FIGURE 126**5'3' Frame 1**

QVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFHSCFGVRMDMLKPSTQN
YKQVKRGNQVLRCLTCTRCKEFLKSVTFRIMVKMLLYQKE--MSQSILNCVNT-IHLL
-LYPPT-ELFTLV

5'3' Frame 2

RFIKMCVFCD-SFT--LCRDNKVTRFVSDFKSGQGYN-LC-NFIHALV-GWTC-NLLPKT
TSKSSVATRCCDA-LVQDAKNAS-KV-PSELW-KCCYTKRNNDECRKVYSTVSILKYTYF
SCTLQHESYSLWCW

5'3' Frame 3

GSSKCVCSVIDLLLLDDFVEIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVETFYPKL
QASQAWQPGVAMPNLYKMQRMLLEKCDLQNYGENAVIPKGIMMNVAKYTQLCQYLNTLTL
AVPSNMRVIHFGAG

3'5' Frame 1

PAPK-ITLMLEGTAKVSVFKY-HS-VYFATFIIIPFGITAFSP-F-RSHFSRSILCILYK
LGIATPGCHA-LACSFG-KVSTCPSLHQSMNEISA-SIVTLTTFEITDKSCDFIISTKSS
SKRSITEHTHFDEP

3'5' Frame 2

QHQSE-LSCWRVQLK-VYLSIDTVEYTLRHSSLFLLV-QHFHHNSEGHTFQEAFASCTS
-ASQHLVATLDLLVVLGRRFQHVHPYTKA-MKFQHSQ-L-P-PLLKSLTNLVTLLSRQSHQ
VKDQSQNTHILMNL

3'5' Frame 3

STKVNNSHVGGYS-SKCI-VLTQLSILCDIHHYSFWYNSIFTIILKVTLFKKHSLHLVQV
RHRNTWLPRLTCL-FWVEGFNMSILTPKHE-NFSIVNCNLDHF-NH-QIL-LYYLDKVIK
-KINHRTHTF-T

FIGURE 127**5'3' Frame 1**

-VFTYPGKANQPRSLVDLFSKRTN-NV--WTPIKPT-CPHYIWWTHRFN-Q-PEWRTAM
GQGONSADPKVYPIILRLGSQLSLSMARRNLDSEARAFQSTPIVVQMTKLATTEELPDE
FVVVTAK-KSSAPDGTSIT-ELAQKLHFPTALTKKASYGLQLREP-IHPKTTLAPAILIT
MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQLLAAGVEILLLEWLAE
VVKLPSRYCC-TD-TSLRAKFLVKANNKAKLSLRNLLLRHLKSLAKNVLPQNSTTSLKH
LGDVVQNKPKAISGTTK-SDKELITNIGPQIAQFA

5'3' Frame 2

RFLPTQEKPTNLDLL-ICSLNEQIKMSDNGPQSNQORSAPRITFGGPTDSTDNNQNGGLQW
GKAKTAPTPTFTQ-YCVLVHSSSHSAWQGGT-IPSRPGRSNQHQ-WSR-PNWLLPKSYPTS
SWW-RQNERAQPQMVLLLPRNWPRSFTSLRR-QRRHRMGCN-GSLEYTQRPHWHPQS--Q
CCHRAATSSRNIAKRLLRGKQRRQSSSLFSLIT-SR-FKKFNSWQQ-GKFSCSNG-RR
W-NCPRAIARQIEPA-EQSFW-RPTTTRPNCH-EICC-GI-KASPKTYCHKTVQRHSSI
WETWSRTNPRKFRGPRPNQTRN-LQTLGRKLHNLP

5'3' Frame 3

GFYLPRKSQPTSISCRSVL-TNKLKCLIMDPNQTNVPPALHLVDPQIQLTITRMEDCNG
ARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPIINTNSGPDDQIGYYRRATRVR
RGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN
AATVLQLPQGTTLPKGFYAEGSRGGSQASSRSSRSRGNSTPGSSRGNSPARMASGG
GETALALLLLDRLNQLESKVSQKQGGQGGQTVTKKSAAEASKKPRQKRTATKQYNVTQAF
GRRGPEQTQGNFGDQDLIRQGTQDYKHWAANCTIC

3'5' Frame 1

RQIVQFAAQCL-SVPCLIRSWSPKFPWVCSGPRLPNA-VTLYCFVAVRFWRGFLDASAAD
FLVTVPCCCWPLPETLLSSWFNLSSSNSARAVSPPLAIRAGEFPLLLPGVEFLELPRL
RDEEREEA-LPPLLPSA-KPFGNVVP-GSCSTVAALLLGLRVPMWSLGVFKAPSVATHM
PSLLAP-GSEASGPVPR--KYHLGLSSFILPSPPRTRRVALR--PIWSSGPLLVLIGTPW
PRGNLSSSLPC-VRAVNQDAILLGKPWGRRCFGLAPLQSSILVIVS-ICGSTKCNAGGTT
LV-LGSIIRHFNLFV-RTDLQEIEVGWFLGR-KP

3'5' Frame 2

GKLCNLRPNVCNQFLV-LGLGPRNFLGFVLDHVSQMLE-RCTVLWQYVFGEAF-MPQQQI

S--QFGLVVVGLYQKLC SQAGSICLAAIARGQFHHLR-PFEQENFPYCCQELNFLNYR DY
 VMRSEKRLDCRLCFPLRRSLLAMLFLEEVVARWQH CY-DCGCQCGLWVYSRLPQLQPIRC
 LLC-RRREVKLLGQFLGNRSTIWG-ALSF CRHHHEL VG-LFGSSQFGHLDHYWC-LERPG
 LEGI-VPPCHAE-EL-TKTQYYWVNLGVGAVLALPHCSPPFWLLSVESVGPPNVMRGALR
 WFDWGPLSDILICSFREQIYKRSRLVGF SWVGKNL

3'5' Frame 3

ANCAICGPMFVISSLS D-VLVPEISLGLFWTTSPKCLSDVVLFCGSTFLARLFRCLSSRF
 LSDSLALLLLAFTRN FALKLVQSV-QQ-REGSFTTSASHSSRRISPTAARS-IS-ITATT
 --GARRGLTAASASLCVEAFWQCCSLRKL-HGGSIVIRIAGANVVF GCIQGSLS CNPYDA
 FFVSAVGK-SFWASS-VIEVPSGAELFHFAVTTTNSSGSSSVVANLVIWTTIGVDWNALA
 SRESKFL LAMLESCEPRRNIIG-TLGSALFWPCPIAVLHSGYCQLNLVWHQM-CGGHYV
 GLIGVHYQTF-FVRL ENRSTRDRGWLA FPG-VKT

FIGURE 128

-GLELKL-LTSICAF-PFCYSLF--CLLYFGFH SKSRI-KNLVPKSKRT-NFSLF-LVFL
 YAVAYAL-YSAVHLINLMCLKILVRYNTRGNTYSTAWLCALGKVL PPHRWHTMVQTCTPN
 VTINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN-NV--WTPIKPT-CPPHYI
 WWTHRFN-Q-PEWRTQWGKAKTAPT PRFTQ-YCVLVHSSHS AWQGGT-IPSRPGRSNQH Q
 -WSR-PNWLLPKSYPTSSWW-RQNERAQPQMVLLLPRNWPRSFTSLRR-QRRHRMGCN-G
 SLEYTQRPHWHPQS--QCCHRATTSSRN NIAKRLLRGKQRRQSSLFSLIT-SR-FKKF
 NSWQQ-GKFSCSNG-RRW-NC PRAIAARQIEPA-EQSFWRPTTTRPNCH-EICC-GI-K
 ASPKTYCHKTVQRHSSIWETWSRTNPRKFRGPRPNQTRN-LQTLAANCTICSKCLCILWN
 VTHWHGSHTFGNMADLSWSH-IG-QRSTIQRQRHTAEQAH-RIQNIPTNRA-KGQKEKD-
 -SSAFAAETKEAAHCDSSSC

EDSSSSFN-LLFVLFSLSAIPCFNNAYYILVFTRNPGSRRTLYQSLNEHETSHCFDLYFS
 MQLHMH CSTALCI--TSCA-RSL-GTTLGVILIALLG FVL-ERFYLFIDGTLWFKHAHLM
 LLSTVKIQLVVRL-LGVGTFMKVTKLLHLETYLLF-INEQIKMSDNGPQSNQRSAPRITF
 GGPTDSTDNNQNGGRNGARPKQRRPQGLPNNIASWFTALTQH GKEELRFPRGQGVPI NTN
 SGPDDQIGYYRRATRRVRGGDGKMKELSPRWYFY YLGTGPEASLPYGANKEGIVWVATEG
 ALNTPKDHIGTRNPNNNAATVLQLPQGTTL PKGFYAEGSRGGSQASSRSSSRSGNSRNS
 TPGSSRGNSPARMASGGGETALALLLLDRLNQLESKVS GKGQQQQGQTVTKKSAAEASKK
 PRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGT DYKHWPOIAQFAPSASAFFGM
 SRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDAYKTFPPTEPKKDKKKKTD
 EAQPLPQRQKKQPTVTLLP

RTRAQALIDFYLCFLAFLFLVLIMLIIFWFSLEIQDLEEPCTKV-TNMKLLIVLTCISL
 CSCICTVVQRCASNKPHVLEDPCVKQH-G-YL-HCLALCSRKGFTFS-MAHYGSNMHT-C
 YYQLSRSSWWCAYS-VLVPS-RSPNCCI-RRTCCFK-TNKLKCLIMDPNQTNVVPPALHL
 VDPQIQLTITRMEAMGQONSADPKVYPIILRLGSQLSLSMARRNLDSEARAFQSTPI
 VVQMTKLATTEELPDEFVVVTAK-KSSAPDGTSTIT-ELAQKLHFPTALTKKASYGLQIRE
 P-IHPKTTLAPAILITMLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQ
 LLAARGEILLLEWLAEVVKLPSRYCC-TD-TSLRAKFLVKANNNKAKLSLRNLLLRHLKS
 LAKNVLPQNSTTSLKHLGDVVQNKPKKEISGTKT-SDKELITNIGRKLHNLLQVPLHSLEC
 HALAWKSHLREHG-LIMEPLNWMTKIHNSKTTSTYC-TSTLTHTKHSQQSLKRTKRKRLM
 KLSLCRRDKRSSPL-LFFL

FIGURE 129

5'3' Frame 1

taccgtagactcatctctatgatggggtttcaaaatgaattaccaagtcaatgggttaccct
 Y R R L I S M M G F K M N Y Q V N G Y P
 aatatgtttatcacccgcgaagaagctattcggtcacgttcgtgcgtggattggctttgat
 N M F I T R E E A I R H V R A W I G F D
 gtagagggtgtcatgcaactagagatgctgtgggtactaacctacctctccagctagga
 V E G C H A T R D A V G T N L P L Q L G
 ttttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataac
 F S T G V N L V A V P T G Y V D T E N N
 acagaattcaccagaggttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
 T E F T R V N A K P P P G D Q F K H L I

5'3' Frame 2

taccgtagactcatctctatgatggggtttcaaaatgaattaccaagtcaatgggttacccta
 T V D S S L - W V S K - I T K S M V T L
 atatgtttatcacccgcgaagaagctattcggtcacgttcgtgcgtggattggctttgatg
 I C L S P A K K L F V T F V R G L A L M
 tagagggtgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggat
 - R A V M Q L E M L W V L T Y L S S - D
 ttttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataaca
 F L Q V L T - - L Y R L V M L T L K I T
 cagaattcaccagaggttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
 Q N S P E L M Q N L H Q V T S L N I L Y

5'3' Frame 3

taccgtagactcatctctatgatggggtttcaaaatgaattaccaagtcaatgggttaccctaa
P - T H L Y D G F Q N E L P S Q W L P -
tatgtttatcacccgcgaagaagctatttcgtcacggttcgtgcggtggattggctttgatgt
Y V Y H P R R S Y S S R S C V D W L - C
agagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggatt
R G L S C N - R C C G Y - P T S P A R I
ttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataacac
F Y R C - L S S C T D W L C - H - K - H
agaattcaccagaggttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
R I H Q S - C K T S T R - P V - T S Y T

3'5' Frame 1

ggtataagatgttttaaactgggtcacctgggtggagggttttgcattaactctggtgaattct
G I R C L N W S P G G G F A L T L V N S
gtgttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaa
V L F S V S T - P V G T A T K L T P V E
aatcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctct
N P S W R G R L V P T A S L V A - Q P S
acatcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacata
T S K P I H A R T - R I A S S R V I N I
ttagggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
L G - P L T W - F I L K P I I E M S L R

3'5' Frame 2

ggtataagatgttttaaactgggtcacctgggtggagggttttgcattaactctggtgaattctg
V - D V - T G H L V E V L H - L W - I L
tggtatttttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaa
C Y F Q C Q H N Q S V Q L L S - H L - K
atcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctcta
I L A G E V G - Y P Q H L - L H D S P L
catcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatat
H Q S Q S T H E R D E - L L R G - - T Y
tagggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
- G N H - L G N S F - N P S - R - V Y G

3'5' Frame 3

ggtataagatggttaaactgggtcacctgggtggaggttttgcattaactctgggtgaattctgt
Y K M F K L V T W W R F C I N S G E F C
gttatttttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaa
V I F S V N I T S R Y S Y - V N T C R K
tcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctac
S - L E R - V S T H S I S S C M T A L Y
atcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatatt
I K A N P R T N V T N S F F A G D K H I
agggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
R V T I D L V I H F E T H H R D E S T V

FIGURE 130

	10	20	30	40	50	60
SEQ ID NO: 9997	KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVR	AWIGFDVEGCHATRDAVGTNLP				
SEQ ID NO:10034	----YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVR	AWIGFDVEGCHATRDAVGTNLP				

Prim. Cons.	KGHD2RRLISMMGFKMNYQVNGYPNMFITREEAIRHVR	AWIGFDVEGCHATRDAVGTNLP				
	70	80	90	100	110	120
SEQ ID NO: 9997	LQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNV	VRIKI				
SEQ ID NO:10034	LQLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLI-----					
	*****:*****:.....:*****					
Prim. cons.	LQLGFSTGVNLVAVPTGYVDTENNT2FTRVNA22222QFKHLIPLMYKGLPWNV	VRIKI				
	130	140	150	160	170	180
SEQ ID NO: 9997	VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD	TYAC				
SEQ ID NO:10034	-----					
Prim. cons.	VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSD	TYAC				
	190	200				
SEQ ID NO: 9997	WNHSVGFQDYVYNPFMIDVQQWGLYG					
SEQ ID NO:10034	-----					

FIGURE 131**5'3' Frame 1**

caggttcatcaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgaga
Q V H Q N V C V L - L I F Y L M T L S R
taataaagtcacaagatttgtcagtgatttcaaaagtggtcaaggttacaattgactatg
- - S H K I C Q - F Q K W S R L Q L T M
ctgaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaac
L K F H S C F G V R M D M L K P S T Q N
tacaagcaagtcaagcgtggcaaccagggtgttgcatgcctaacttgtacaagatgcaaa
Y K Q V K R G N Q V L R C L T C T R C K
gaatgcttcttgaaaagtggtgaccttcagaattatggtgaaaatgctgttataccaaaag
E C F L K S V T F R I M V K M L L Y Q K
gaataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaaatacacttactt
E - - - M S Q S I L N C V N T - I H L L
tagctgtaccctccaacatgagagttattcactttggtgctgg
- L Y P P T - E L F T L V L

5'3' Frame 2

caggttcatcaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagat
R F I K M C V F C D - S F T - - L C R D
aataaagtcacaagatttgtcagtgatttcaaaagtggtcaaggttacaattgactatgc
N K V T R F V S D F K S G Q G Y N - L C
tgaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaact
- N F I H A L V - G W T C - N L L P K T
acaagcaagtcaagcgtggcaaccagggtgttgcatgcctaacttgtacaagatgcaaag
T S K S S V A T R C C D A - L V Q D A K
aatgcttcttgaaaagtggtgaccttcagaattatggtgaaaatgctgttataccaaaagg
N A S - K V - P S E L W - K C C Y T K R
aataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaaatacacttacttt
N N D E C R K V Y S T V S I L K Y T Y F
agctgtaccctccaacatgagagttattcactttggtgctgg
S C T L Q H E S Y S L W C W

5'3' Frame 3

caggttcatcaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagata
G S S K C V C S V I D L L L D D F V E I
ataaagtcacaagatttgtcagtgatttcaaaagtggtcaaggttacaattgactatgct
I K S Q D L S V I S K V V K V T I D Y A
gaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaacta
E I S F M L W C K D G H V E T F Y P K L
caagcaagtcaagcgtggcaaccagggtgttgcatgcctaacttgtacaagatgcaaaga

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Q A S Q A W Q P G V A M P N L Y K M Q R
atgcttcttgaaaagtgtgaccttcagaattatgggtgaaaatgctgttataccaaaaagga
M L L E K C D L Q N Y G E N A V I P K G
ataatgatgaatgtcgcgaaagtataactcaactgtgtcaataacttaaatacacttacttta
I M M N V A K Y T Q L C Q Y L N T L T L
gctgtaccctccaacatgagaggttattcacttttggtgctgg
A V P S N M R V I H F G A

3'5' Frame 1

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaag
P A P K - I T L M L E G T A K V S V F K
tattgacacagttgagtatacttttgcgacattcatcattattccttttgggtataaacagca
Y - H S - V Y F A T F I I I P F G I T A
ttttcaccataaattctgaagggtcacacttttcaagaagcattcctttgcatccttgtaacaag
F S P - F - R S H F S R S I L C I L Y K
ttaggcacgcgaacacctgggttgccacgcttgacttgcttgtagttttgggtagaagggtt
L G I A T P G C H A - L A C S F G - K V
tcaacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacc
S T C P S L H Q S M N E I S A - S I V T
ttgaccacttttgaaatcactgacaaatccttggtgactttattatctcgacaaagtcatca
L T T F E I T D K S C D F I I S T K S S
agtaaaagatcaatcacagaacacacacattttgatgaacctg
S K R S I T E H T H F D E P

3'5' Frame 2

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaagt
Q H Q S E - L S C W R V Q L K - V Y L S
attgacacagttgagtatacttttgcgacattcatcattattccttttgggtataaacagcat
I D T V E Y T L R H S S L F L L V - Q H
tttcaccataaattctgaagggtcacacttttcaagaagcattcctttgcatccttgtaacaag
F H H N S E G H T F Q E A F F A S C T S
taggcacgcgaacacctgggttgccacgcttgacttgcttgtagttttgggtagaagggtt
- A S Q H L V A T L D L L V V L G R R F
caacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacct
Q H V H P Y T K A - M K F Q H S Q L - P
tgaccacttttgaaatcactgacaaatccttggtgactttattatctcgacaaagtcatcaa
- P L L K S L T N L V T L L S R Q S H Q
gtaaaagatcaatcacagaacacacacattttgatgaacctg
V K D Q S Q N T H I L M N L

3'5' Frame 3

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaagta
 S T K V N N S H V G G Y S - S K C I - V
 ttgacacagttgagtatacttttgcgacattcatcattattccttttgggtataacagcatt
 L T Q L S I L C D I H H Y S F W Y N S I
 ttcaccataattctgaagggtcacactttttcaagaagcattcctttgcatcttgtacaagtt
 F T I I L K V T L F K K H S L H L V Q V
 aggcacgcgaacacctggttgccacgcttgacttgcttgtagttttgggtagaaggtttc
 R H R N T W L P R L T C L - F W V E G F
 aacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcattgtaacctt
 N M S I L T P K H E - N F S I V N C N L
 gaccacttttgaaatcactgacaaatccttgtagctttattatctcgacaaagtcacaaag
 D H F - N H - Q I L - L Y Y L D K V I K
 taaaagatcaatcacagaacacacacattttgatgaacctg
 - K I N H R T H T F - - T

FIGURE 132**5'3' Frame 1**

taggtttttacctaccaggaagccaaccaacctcgatctctttagatctgttctct
 - V F T Y P G K A N Q P R S L V D L F S
 aaacgaacaaattaaaatgtctgataatggaccccaatcaaaccaacgtagtgcccccg
 K R T N - N V - - W T P I K P T - C P P
 cattacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatg
 H Y I W W T H R F N - Q - P E W R T A M
 gggcaaggccaaaacagcgccgaccccaagggtttaccaataatattgcgtcttgggttca
 G Q G Q N S A D P K V Y P I I L R L G S
 cagctctcactcagcatggcaaggaggaacttagattccctcgaggccagggcggttccaa
 Q L S L S M A R R N L D S L E A R A F Q
 tcaacaccaatagtgtccagatgaccaaattggctactaccgaagagctacccgacgag
 S T P I V V Q M T K L A T T E E L P D E
 ttcgtgggtggtgacggcaaaatgaaagagctcagccccagatggtagcttctattacctag
 F V V V T A K - K S S A P D G T S I T -
 gaactggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtaggggttg
 E L A Q K L H F P T A L T K K A S Y G L
 caactgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataaca
 Q L R E P - I H P K T T L A P A I L I T
 atgctgccaccgtgctacaacttctcaaggaacaacattgccaaaaggcttctacgcag
 M L P P C Y N F L K E Q H C Q K A S T Q
 agggaagcagaggcggcagtcagcctcttctcgtcctcatcacgtagtcgcggtaatt
 R E A E A A V K P L L A P H H V V A V I
 caagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggag
 Q E I Q L L A A V G E I L L L E W L A E

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gtggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaag
V V K L P S R Y C C - T D - T S L R A K
tttctggttaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgagg
F L V K A N N N K A K L S L R N L L L R
catctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcat
H L K S L A K N V L P Q N S T T S L K H
ttgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagac
L G D V V Q N K P K E I S G T K T - S D
aaggaactgattacaaacattggggccgcaaattgcacaatttgcct
K E L I T N I G P Q I A Q F A

5'3' Frame 2

taggtttttacctaccagggaaaagccaaccaacctcgatctctttagatctgttctcta
R F L P T Q E K P T N L D L L - I C S L
aacgaacaaattaaaatgtctgataatggacccaatcaaaccaacgtagtgtccccgc
N E Q I K M S D N G P Q S N Q R S A P R
attacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatgg
I T F G G P T D S T D N N Q N G G L Q W
ggcaaggccaaaacagcgccgacccaagggtttaccaataatattgcgtcttggttcac
G K A K T A P T P R F T Q - Y C V L V H
agctctcactcagcatggcaaggaggaacttagattccctcgaggccaggcggtccaat
S S H S A W Q G G T - I P S R P G R S N
caacaccaatagtgggtccagatgaccaaattgggtactaccgaagagctacccgacgagt
Q H Q - W S R - P N W L L P K S Y P T S
tcgtgggtgggtgacggcaaaatgaaagagctcagccccagatgggtacttctattacctagg
S W W - R Q N E R A Q P Q M V L L L P R
aactggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtatgggttgc
N W P R S F T S L R R - Q R R H R M G C
aactgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataacaa
N - G S L E Y T Q R P H W H P Q S - - Q
tgctgccaccgtgctacaacttcctcaaggaacaacattgccaaaaggcttctacgcaga
C C H R A T T S S R N N I A K R L L R R
gggaagcagaggcggcagtcagcctcttctcgtcctcatcacgtagtcgcggtaattc
G K Q R R Q S S L F S L L I T - S R - F
aagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggagg
K K F N S W Q Q - G K F S C S N G - R R
tggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagt
W - N C P R A I A A R Q I E P A - E Q S
ttctggtaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggc
F W - R P T T T R P N C H - E I C C - G
atctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcatt
I - K A S P K T Y C H K T V Q R H S S I
tgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagaca
W E T W S R T N P R K F R G P R P N Q T
aggaactgattacaaacattggggccgcaaattgcacaatttgcct
R N - L Q T L G R K L H N L P

5'3' Frame 3

taggttttttacctacccaggaaaagccaaccaacctcgatctctttagatctgttctctaa
G F Y L P R K S Q P T S I S C R S V L -
acgaacaaattaaaatgtctgataatggaccccaatcaaaccaacgtagtgcccccgca
T N K L K C L I M D P N Q T N V V P P A
ttacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatggg
L H L V D P Q I Q L T I T R M E D C N G
gcaaggccaaaacagcgccgaccccaagggtttacccaataatattgcbtcttggttcaca
A R P K Q R R P Q G L P N N I A S W F T
gctctcactcagcatggcaaggaggaacttagattccctcgaggccagggcggttccaatc
A L T Q H G K E E L R F P R G Q G V P I
aacaccaatagtgggtccagatgaccaaattggctactaccgaagagctacccgacgagtt
N T N S G P D D Q I G Y Y R R A T R R V
cgtgggtggtgacggcaaaatgaaagagctcagccccagatgggtacttctattacctagga
R G G D G K M K E L S P R W Y F Y Y L G
actggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtaggggttga
T G P E A S L P Y G A N K E G I V W V A
actgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataacaat
T E G A L N T P K D H I G T R N P N N N
gctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcagag
A A T V L Q L P Q G T T L P K G F Y A E
ggaagcagaggcggcagtcagcctcttctcgctcctcatcacgtagtcgcggttaattca
G S R G G S Q A S S R S S S R S R G N S
agaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggaggt
R N S T P G S S R G N S P A R M A S G G
ggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagtt
G E T A L A L L L L D R L N Q L E S K V
tctggttaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggca
S G K G Q Q Q Q G Q T V T K K S A A E A
tctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcattt
S K K P R Q K R T A T K Q Y N V T Q A F
gggagacgtgggtccagaacaaacccaaggaaatttctggggaccaagacctaatacagacaa
G R R G P E Q T Q G N F G D Q D L I R Q
ggaactgattacaaacattggggccgcaaattgcacaatttgcct
G T D Y K H W A A N C T I C

3'5' Frame 1

aggcaaatgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtct
R Q I V Q F A A Q C L - S V P C L I R S
tggtccccgaaatttcccttgggtttgttctggaccacgtctcccaaattgcttgagtgcg
W S P K F P W V C S G P R L P N A - V T
ttgtactgttttgtggcagtagcttttggcgaggctttttagatgcctcagcagcagat

L Y C F V A V R F W R G F L D A S A A D
ttcttagtgacagtttggccttggtgttggtggcctttaccagaaactttgctctcaagc
F L V T V W P C C C W P L P E T L L S S
tggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccatt
W F N L S S S N S A R A V S P P P L A I
cgagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgacta
R A G E F P L L L P G V E F L E L P R L
cgtgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcct
R D E E R E E A - L P P L L P S A - K P
tttggcaatgttggtccttgagggaagttgtagcacggtggcagcattgttattaggattg
F G N V V P - G S C S T V A A L L L G L
cgggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaaccatacgatg
R V P M W S L G V F K A P S V A T H T M
ccttctttgttagcgccgtagggaagtgagcttctgggccagttccttaggtaatagaag
P S L L A P - G S E A S G P V P R - - K
taccatctggggctgagctctttcattttgccgtcaccaccacgaactcgtcgggtagct
Y H L G L S S F I L P S P P R T R R V A
cttcggtagtagccaatttggtcatctggaccactattggtgttgattggaacgccctgg
L R - - P I W S S G P L L V L I G T P W
cctcgagggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgca
P R G N L S S S L P C - V R A V N Q D A
atattattgggttaaacccttggggctcggcgtgttttggccttgccccattgcagtcctcc
I L L G K P W G R R C F G L A P L Q S S
attctggttattgtcagttgaatctgtgggtccaccaaagtgaatgcggggggactacg
I L V I V S - I C G S T K C N A G G T T
ttggtttgattgggggtccattatcagacatttttaatttggttcgtttagagaacagatcta
L V - L G S I I R H F N L F V - R T D L
caagagatcgaggttggttggttttctgggttaggtaaaaacctta
Q E I E V G W L F L G R - K P

3'5' Frame 2

aggcaaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtctt
G K L C N L R P N V C N Q F L V - L G L
gggtccccgaaatttcccttgggtttgttctggaccacgtctcccaaagtgttgagtacgt
G P R N F L G F V L D H V S Q M L E - R
tgtactgttttgtggcagtagcttttggcgaggcttttttagatgcctcagcagcagatt
C T V L W Q Y V F G E A F - M P Q Q Q I
tcttagtgacagtttggccttggtgttggtggcctttaccagaaactttgctctcaagct
S - - Q F G L V V V G L Y Q K L C S Q A
gggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccattc
G S I C L A A I A R G Q F H H L R - P F
gagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactac
E Q E N F P Y C C Q E L N F L N Y R D Y
gtgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcctt
V M R S E K R L D C R L C F P L R R S L
ttggcaatgttggtccttgagggaagttgtagcacggtggcagcattgttattaggattgc

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L A M L F L E E V V A R W Q H C Y - D C
gggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaacccatac gatgc
G C Q C G L W V Y S R L P Q L Q P I R C
cttctttgttagcgccgtaggggaagtgaagcttctgggccagttcctaggtaatagaagt
L L C - R R R E V K L L G Q F L G N R S
accatctggggctgagctctttcattttgccgtcaccaccacgaactcgtcgggtagctc
T I W G - A L S F C R H H H E L V G - L
ttcggtagtagccaatttgggtcatctggaccactattgggtgttgattggaacgccctggc
F G S S Q F G H L D H Y W C - L E R P G
ctcgaggggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaa
L E G I - V P P C H A E - E L - T K T Q
tattattgggtaaacccttggggctggcgctgttttggccttgccccattgcagtcctcca
Y Y W V N L G V G A V L A L P H C S P P
ttctgggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacgt
F W L L S V E S V G P P N V M R G A L R
tggtttgattgggggtccattatcagacattttaatttggttcgtttagagaacagatctac
W F D W G P L S D I L I C S F R E Q I Y
aagagatcgaggttggttggcttttctgggttaggtaaaaaccta
K R S R L V G F S W V G K N L

3'5' Frame 3

aggcaaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtcttg
A N C A I C G P M F V I S S L S D - V L
gtccccgaaatttcttgggtttgttctggaccacgtctcccaaatagttgagtgcgtt
V P E I S L G L F W T T S P K C L S D V
gtactgttttgtggcagtagctttttggcgaggcttttttagatgcctcagcagcagattt
V L F C G S T F L A R L F R C L S S R F
cttagtgacagtttggccttgttgttggcctttaccagaaactttgctctcaagctg
L S D S L A L L L L A F T R N F A L K L
gttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccattcg
V Q S V - Q Q - R E G S F T T S A S H S
agcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactacg
S R R I S P T A A R S - I S - I T A T T
tgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagccttt
- - G A R R G L T A A S A S L C V E A F
tggcaatgttggtccttgaggaagttgtagcacggtggcagcattgttattaggattgcg
W Q C C S L R K L - H G G S I V I R I A
ggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaacccatac gatgcc
G A N V V F G C I Q G S L S C N P Y D A
ttctttgttagcgccgtaggggaagtgaagcttctgggccagttcctaggtaatagaagta
F F V S A V G K - S F W A S S - V I E V
ccatctggggctgagctctttcattttgccgtcaccaccacgaactcgtcgggtagctct
P S G A E L F H F A V T T T N S S G S S
tcggtagtagccaatttgggtcatctggaccactattgggtgttgattggaacgccctggcc
S V V A N L V I W T T I G V D W N A L A
tcgaggggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaat

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S R E S K F L L A M L S E S C E P R R N
attattgggtaaacccttgggggtcggcgctgttttggccttgccccattgcagtcctccat
I I G - T L G S A L F W P C P I A V L H
tctgggttattgtcagttgaatctgtgggtccaccaaataatgcgggggggcactacgtt
S G Y C Q L N L W V H Q M - C G G H Y V
ggtttgattgggggtccattatcagacattttaatttggttcgttttagagaacagatctaca
G L I G V H Y Q T F - F V R L E N R S T
agagatcgaggttgggttggttttctgggtaggtaaaaaccta
R D R G W L A F P G - V K T

FIGURE 133

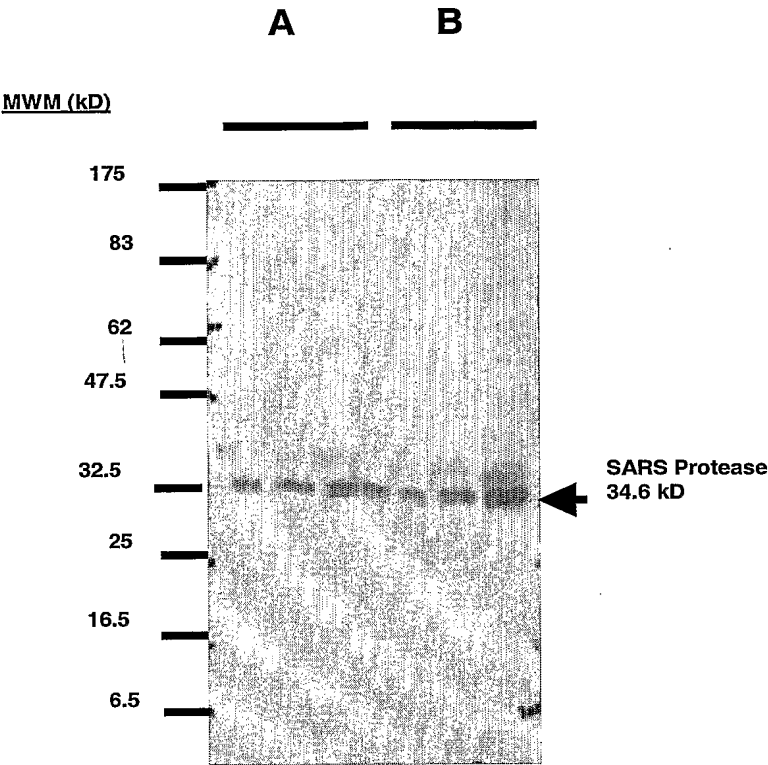


FIGURE 134